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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds  
(without alignments)  
28.022 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	57.7	10	4	US-09-535-852-1357 Sequence 1357, Ap
2	15	57.7	10	4	US-09-535-852-1366 Sequence 1366, Ap
3	15	57.7	10	4	US-09-535-852-1375 Sequence 1375, Ap
4	15	57.7	10	4	US-09-535-852-1385 Sequence 1385, Ap
5	15	57.7	10	4	US-09-535-852-1395 Sequence 1395, Ap
6	15	57.7	10	4	US-09-535-852-1825 Sequence 1825, Ap
7	15	57.7	10	4	US-09-535-852-1829 Sequence 1829, Ap
8	15	57.7	10	4	US-09-535-852-1833 Sequence 1833, Ap
9	14	53.8	10	2	US-08-764-640-77 Sequence 77, Appl
10	14	53.8	10	3	US-08-973-225-77 Sequence 77, Appl
11	14	53.8	10	3	US-09-244-298A-77 Sequence 77, Appl
12	14	53.8	10	3	US-09-516-704-77 Sequence 77, Appl
13	14	53.8	10	3	US-09-187-859-3644 Sequence 3644, Ap
14	14	53.8	10	3	US-09-187-859-3646 Sequence 3646, Ap
15	14	53.8	10	4	US-09-549-090-77 Sequence 77, Appl
16	14	53.8	10	4	US-09-832-230A-77 Sequence 77, Appl
17	14	53.8	10	4	US-09-839-542B-3644 Sequence 3644, Ap
18	14	53.8	10	4	US-09-839-542B-3646 Sequence 3646, Ap
19	14	53.8	10	4	US-09-535-852-1352 Sequence 1352, Ap
20	14	53.8	10	4	US-09-535-852-1361 Sequence 1361, Ap
21	14	53.8	10	4	US-09-535-852-1370 Sequence 1370, Ap
22	14	53.8	10	4	US-09-535-852-1380 Sequence 1380, Ap
23	14	53.8	10	4	US-09-535-852-1390 Sequence 1390, Ap
24	14	53.8	10	4	US-09-620-091-49 Sequence 49, Appl
25	13	50.0	10	2	US-08-764-640-102 Sequence 102, App
26	13	50.0	10	2	US-08-764-640-120 Sequence 120, App
27	13	50.0	10	2	US-08-764-640-121 Sequence 121, App

28	13	50.0	10	3	US-08-925-002-67 Sequence 67, Appl
29	13	50.0	10	3	US-08-973-225-102 Sequence 102, App
30	13	50.0	10	3	US-08-973-225-120 Sequence 120, App
31	13	50.0	10	3	US-08-973-225-121 Sequence 121, App
32	13	50.0	10	3	US-08-973-225-207 Sequence 207, App
33	13	50.0	10	3	US-08-973-225-208 Sequence 208, App
34	13	50.0	10	3	US-08-377-781A-17 Sequence 17, Appl
35	13	50.0	10	3	US-08-377-781A-18 Sequence 18, Appl
36	13	50.0	10	3	US-09-244-298A-102 Sequence 102, App
37	13	50.0	10	3	US-09-244-298A-120 Sequence 120, App
38	13	50.0	10	3	US-09-244-298A-121 Sequence 121, App
39	13	50.0	10	3	US-09-516-704-102 Sequence 102, App
40	13	50.0	10	3	US-09-516-704-120 Sequence 120, App
41	13	50.0	10	3	US-09-516-704-121 Sequence 121, App
42	13	50.0	10	3	US-09-187-859-834 Sequence 834, App
43	13	50.0	10	3	US-09-187-859-836 Sequence 836, App
44	13	50.0	10	3	US-09-187-859-1075 Sequence 1075, Ap
45	13	50.0	10	3	US-09-187-859-1077 Sequence 1077, Ap

ALIGNMENTS

RESULT 1  
US-09-535-852-1357  
; Sequence 1357, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1357  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence  
US-09-535-852-1357

Query Match 57.7%; Score 15; DB 4; Length 10;  
Best Local Similarity 20.0%; Pred. No. 15;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
Db 1 CAYATTADGC 10

RESULT 2  
US-09-535-852-1366  
; Sequence 1366, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1366  
; LENGTH: 10

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1366

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
      |
Db      1 CYAYATTAC 10

RESULT 3
US-09-535-852-1375
; Sequence 1375, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1375
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1375

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
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Db      1 CLYAYATTAC 10

RESULT 4
US-09-535-852-1385
; Sequence 1385, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1385
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1385
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Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
      |
Db      1 CVYAYATTAC 10

RESULT 5
US-09-535-852-1395
; Sequence 1395, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1395
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1395

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
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Db      1 CIYAYATTAC 10

RESULT 6
US-09-535-852-1825
; Sequence 1825, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1825
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-535-852-1825

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
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Db 1 CAYASTADGC 10

RESULT 7

US-09-535-852-1829

; Sequence 1829, Application US/09535852

; Patent No. 6638911

; GENERAL INFORMATION:

; APPLICANT: Symonds, James M.

; APPLICANT: Blachuk, Orest W.

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING

; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C6

; CURRENT APPLICATION NUMBER: US/09/535,852

; CURRENT FILING DATE: 2001-05-21

; NUMBER OF SEQ ID NOS: 2009

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1829

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Cyclicized modulating agent comprising

; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion

; OTHER INFORMATION: recognition sequence

US-09-535-852-1829

Query Match 57.7%; Score 15; DB 4; Length 10;

Best Local Similarity 20.0%; Pred. No. 15;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 1 CIAYASTADC 10

RESULT 8

US-09-535-852-1833

; Sequence 1833, Application US/09535852

; Patent No. 6638911

; GENERAL INFORMATION:

; APPLICANT: Symonds, James M.

; APPLICANT: Blachuk, Orest W.

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING

; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C6

; CURRENT APPLICATION NUMBER: US/09/535,852

; CURRENT FILING DATE: 2001-05-21

; NUMBER OF SEQ ID NOS: 2009

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1833

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Cyclicized modulating agent comprising

; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion

; OTHER INFORMATION: recognition sequence

US-09-535-852-1833

Query Match 57.7%; Score 15; DB 4; Length 10;

Best Local Similarity 20.0%; Pred. No. 15;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 1 CLIAYASTAC 10

RESULT 9

US-08-764-640-77

; Sequence 77, Application US/08764640

; Patent No. 5869451

; Patent No. 5869451 5837683

; GENERAL INFORMATION:

; APPLICANT: Dower, William J.

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Cwirla, Steven E.

; APPLICANT: Gates, Christian

; APPLICANT: Schatz, Peter J.

; APPLICANT: Balasubramanian, Palaniappan

; APPLICANT: Wagstrom, Christopher R.

; APPLICANT: Hendren, Richard W.

; APPLICANT: Deprince, Randolph B.

; APPLICANT: Podduturi, Surekha

; APPLICANT: Yin, Qun

; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

; TITLE OF INVENTION: RECEPTOR

; NUMBER OF SEQUENCES: 244

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Glaxo Wellcome

; STREET: Five Moore Drive, P.O. Box 13398

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/764,640

; FILING DATE: 11-DEC-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Hrubiec, Robert T.

; REGISTRATION NUMBER: 36,392

; REFERENCE/DOCKET NUMBER: PK3281

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-248-1000

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-764-640-77

Query Match 53.8%; Score 14; DB 2; Length 10;

Best Local Similarity 20.0%; Pred. No. 69;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 1 CSRADFLAAC 10

RESULT 10

US-08-973-225-77

; Sequence 77, Application US/08973225A

; Patent No. 6083913

; GENERAL INFORMATION:

; APPLICANT: Dower, William J.

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Cwirla, Steven E.

; APPLICANT: Duffin, David J.

; APPLICANT: Gates, Christian

; APPLICANT: Haselden, Sherril S.

; APPLICANT: Mattheakis, Larry C.

; APPLICANT: Schatz, Peter J.

; APPLICANT: Wagstrom, Christopher R.

; APPLICANT: Wrighton, Nicholas C.

;  
;  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
;  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
;  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/973,225A  
; FILING DATE: 04-Dec-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
;  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
;  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
;  
; MOLECULE TYPE: peptide  
;  
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-08-973-225-77  
  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 69;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
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Db 1 CSRADFLAAC 10  
  
RESULT 11  
US-09-244-298A-77  
; Sequence 77, Application US/09244298A  
; Patent No. 6121238  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
;  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/516,704  
; FILING DATE: 01-Mar-2000  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
;  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
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; STRANDEDNESS:  
; TOPOLOGY: linear  
;  
; MOLECULE TYPE: peptide  
;  
; MISC. INFORMATION:  
; MISC. INFORMATION:  
US-09-244-298A-77

;  
;  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/244,298A  
; FILING DATE: 11-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
;  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
;  
; MOLECULE TYPE: peptide  
;  
; MISC. INFORMATION:  
; MISC. INFORMATION:  
US-09-244-298A-77  
  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 69;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
|  
Db 1 CSRADFLAAC 10  
  
RESULT 12  
US-09-516-704-77  
; Sequence 77, Application US/09516704  
; Patent No. 6251864  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
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; SOFTWARE: PatentIn Release #1.0, Version #1.30  
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/516,704  
; FILING DATE: 01-Mar-2000  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
;  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
;  
; STRANDEDNESS:  
; TOPOLOGY: linear  
;  
; MOLECULE TYPE: peptide  
;  
; MISC. INFORMATION:  
; MISC. INFORMATION:  
US-09-244-298A-77

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; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-516-704-77

Query Match      53.8%; Score 14; DB 3; Length 10;
Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
Db      1 CSRADFLAAC 10

RESULT 13
US-09-187-859-3644
; Sequence 3644, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3644
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3644

Query Match      53.8%; Score 14; DB 3; Length 10;
Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
Db      1 CFTIDSSGC 10

RESULT 14
US-09-187-859-3646
; Sequence 3646, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3646
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3646

Query Match      53.8%; Score 14; DB 3; Length 10;
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Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
Db      1 CKFTIDSSC 10

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; Sequence 77, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Duffin, David J.
; APPLICANT: Gates, Christian
; APPLICANT: Haselden, Sherril S.
; APPLICANT: Mattheakis, Larry C.
; APPLICANT: Schatz, Peter J.
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,090
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-549-090-77

Query Match      53.8%; Score 14; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
Db      1 CSRADFLAAC 10

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Job time : 23.6667 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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43.869 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15	57.7	10	17	US-10-654-578-1366
3	15	57.7	10	17	US-10-654-578-1375
4	15	57.7	10	17	US-10-654-578-1385
5	15	57.7	10	17	US-10-654-578-1395
6	15	57.7	10	17	US-10-654-578-1825
7	15	57.7	10	17	US-10-654-578-1829
8	15	57.7	10	17	US-10-654-578-1833
9	14	53.8	10	10	US-09-572-404B-2111
10	14	53.8	10	10	US-09-572-404B-2169
11	14	53.8	10	13	US-10-046-922-58
12	14	53.8	10	14	US-10-006-869-3644
13	14	53.8	10	14	US-10-006-869-3646

14	14	53.8	10	14	US-10-083-768-77	Sequence 77, Appl
15	14	53.8	10	14	US-10-395-032-3644	Sequence 3644, Ap
16	14	53.8	10	14	US-10-395-032-3646	Sequence 3646, Ap
17	14	53.8	10	17	US-10-654-578-1352	Sequence 1352, Ap
18	14	53.8	10	17	US-10-654-578-1361	Sequence 1361, Ap
19	14	53.8	10	17	US-10-654-578-1370	Sequence 1370, Ap
20	14	53.8	10	17	US-10-654-578-1380	Sequence 1380, Ap
21	14	53.8	10	17	US-10-654-578-1390	Sequence 1390, Ap
22	13	50.0	10	9	US-09-234-395-220	Sequence 220, App
23	13	50.0	10	9	US-09-234-395-222	Sequence 222, App
24	13	50.0	10	9	US-09-305-928-220	Sequence 220, App
25	13	50.0	10	9	US-09-305-928-222	Sequence 222, App
26	13	50.0	10	9	US-09-264-516A-244	Sequence 244, App
27	13	50.0	10	9	US-09-264-516A-246	Sequence 246, App
28	13	50.0	10	9	US-09-910-552-67	Sequence 67, Appl
29	13	50.0	10	10	US-09-572-404B-1223	Sequence 1223, Ap
30	13	50.0	10	10	US-09-572-404B-1225	Sequence 1225, Ap
31	13	50.0	10	10	US-09-572-404B-1231	Sequence 1231, Ap
32	13	50.0	10	10	US-09-572-404B-1235	Sequence 1235, Ap
33	13	50.0	10	10	US-09-572-404B-1239	Sequence 1239, Ap
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35	13	50.0	10	10	US-09-572-404B-1293	Sequence 1293, Ap
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37	13	50.0	10	10	US-09-572-404B-1309	Sequence 1309, Ap
38	13	50.0	10	10	US-09-572-404B-1335	Sequence 1335, Ap
39	13	50.0	10	10	US-09-572-404B-1337	Sequence 1337, Ap
40	13	50.0	10	10	US-09-572-404B-1417	Sequence 1417, Ap
41	13	50.0	10	10	US-09-572-404B-1427	Sequence 1427, Ap
42	13	50.0	10	10	US-09-572-404B-1451	Sequence 1451, Ap
43	13	50.0	10	10	US-09-572-404B-1489	Sequence 1489, Ap
44	13	50.0	10	10	US-09-572-404B-1505	Sequence 1505, Ap
45	13	50.0	10	10	US-09-572-404B-1521	Sequence 1521, Ap

ALIGNMENTS

RESULT 1  
US-10-654-578-1357  
; Sequence 1357, Application US/10654578  
; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578  
; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1357  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence  
US-10-654-578-1357

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
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Db 1 CAYATTADGC 10

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US-10-654-578-1366  
; Sequence 1366, Application US/10654578



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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-654-578-1825

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 1 CAYASTADGC 10

RESULT 7

US-10-654-578-1829  
; Sequence 1829, Application US/10654578  
; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: 10086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578  
; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1829  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-654-578-1829

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 1 CIAYASTADC 10

RESULT 8

US-10-654-578-1833  
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; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: 10086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578  
; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1833  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-654-578-1825

;  
; OTHER INFORMATION: recognition sequence  
US-10-654-578-1833

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 1 CLIAYASTAC 10

RESULT 9

US-09-572-404B-2111  
; Sequence 2111, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 2111  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in C6 at 873-882 and may interact with Sequence ;  
; OTHER INFORMATION: this patent.  
US-09-572-404B-2111

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Best Local Similarity 20.0%; Pred. No. 4.9e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
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Db 1 CSASTSKVC 10

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; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 2169  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in C6 at 873-882 and may interact with Sequence ;  
; OTHER INFORMATION: this patent.  
US-09-572-404B-2169

Query Match 53.8%; Score 14; DB 10; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.9e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
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Db 1 CSASTSKVC 10

RESULT 11

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US-10-046-922-58
; Sequence 58, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 10
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-58

Query Match          53.8%; Score 14; DB 13; Length 10;
Best Local Similarity 20.0%; Pred. No. 4.9e+02;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 1 CRALDSALAC 10

RESULT 12
US-10-006-869-3644
; Sequence 3644, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3644
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3644

Query Match          53.8%; Score 14; DB 14; Length 10;
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QY 1 CXXXXXXXXC 10
Db 1 CFTIDSSGC 10

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; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
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; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
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; SEQ ID NO 3646
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3646

Query Match          53.8%; Score 14; DB 14; Length 10;
Best Local Similarity 20.0%; Pred. No. 4.9e+02;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 1 CKFTIDSSSC 10

RESULT 14
US-10-083-768-77
; Sequence 77, Application US/10083768
; Publication No. US20030158116A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Duffin, David J.
; APPLICANT: Gates, Christian
; APPLICANT: Haselden, Sherril S.
; APPLICANT: Mattheakis, Larry C.
; APPLICANT: Schatz, Peter J.
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-083-768-77

Query Match          53.8%; Score 14; DB 14; Length 10;
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Best Local Similarity 20.0%; Pred. No. 4.9e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 1 CSRADFLAAC 10

RESULT 15  
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; Sequence 3644, Application US/10395032  
; Publication No. US20030229199A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C9  
; CURRENT APPLICATION NUMBER: US/10/395,032  
; CURRENT FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3644  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-395-032-3644

Query Match 53.8%; Score 14; DB 14; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.9e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 1 CFTIDSSGC 10

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(without alignments)  
50.640 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	34.6	3	A22565	R-phycoerythrin al
2	9	34.6	4	I51049	metallothionein-A
3	9	34.6	4	S43959	Ig mu chain V regi
4	9	34.6	4	S55238	pallidipin - assas
5	9	34.6	5	B22565	R-phycoerythrin al
6	9	34.6	5	F22565	R-phycoerythrin ga
7	9	34.6	5	A33882	cadmium-binding pe
8	9	34.6	5	B45525	actin I - malaria
9	9	34.6	5	S65726	hemoglobin, extrac
10	9	34.6	6	JU0355	lipopeptide WS1279
11	9	34.6	6	C22565	R-phycoerythrin be
12	9	34.6	6	I37027	protamine P1 - gor
13	9	34.6	6	I37263	Y protein - human
14	9	34.6	6	H48394	glycoprotein compo
15	9	34.6	6	I67345	MHC H2-K-k cell su
16	9	34.6	6	I65546	MHC H2-L antigen -
17	9	34.6	6	PT0652	T-cell receptor be
18	9	34.6	6	F41946	T-cell receptor ga
19	9	34.6	6	I49421	laminin B1 - weste
20	9	34.6	6	S29881	Na+/K+-exchanging
21	9	34.6	6	I79564	hypothetical TCL3
22	9	34.6	7	PH1408	Ig heavy chain V r
23	9	34.6	7	S38516	mabinlin II chain
24	9	34.6	7	B34818	vicilin 57K chain
25	9	34.6	7	B33882	cadmium-binding he
26	9	34.6	7	A34026	acetylcholinestera
27	9	34.6	7	A12016	formylglycinamide
28	9	34.6	7	PH1602	Ig H chain V-D-J r
29	9	34.6	7	PH0932	T-cell receptor be

30	9	34.6	7	2	A58512	venom heptapeptide
31	9	34.6	7	2	S08606	hypothetical prote
32	9	34.6	7	4	I56695	hypothetical L2 pr
33	9	34.6	8	2	PH1407	Ig heavy chain V r
34	9	34.6	8	2	S59622	metallothionein is
35	9	34.6	8	2	PH1618	Ig H chain V-D-J r
36	9	34.6	8	2	PH0803	T-cell receptor al
37	9	34.6	8	2	PH0934	T-cell receptor be
38	9	34.6	8	2	PC1002	leucine-tRNA ligas
39	9	34.6	8	2	S19288	acylase - Kluyvera
40	9	34.6	8	2	A37521	R-phycoerythrin ga
41	9	34.6	8	2	C61512	variant surface gl
42	9	34.6	8	2	D61512	variant surface gl
43	9	34.6	8	2	I57018	gene Cfr protein
44	9	34.6	8	2	A25836	L-serine ammonia-1
45	9	34.6	8	2	XGHUEU	urine glycopeptide

ALIGNMENTS

RESULT 1  
A22565  
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: A22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: A22565  
A;Molecule type: protein  
A;Residues: 1-3 <KJO>

Query Match 34.6%; Score 9; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 1 C 1

RESULT 2  
I51049  
metallothionein-A - rainbow trout (fragment)  
C;Species: Oncorhynchus mykiss (rainbow trout)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C;Accession: I51049  
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.  
Eur. J. Biochem. 230, 344-349, 1995  
A;Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) met  
A;Reference number: I51049; MUID:95324545; PMID:7601121  
A;Accession: I51049  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-4 <OLS>  
A;Cross-references: EMBL:X80181; NID:gl019799; PIDN:CAA56466.1; PID:g4379328

Query Match 34.6%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 3  
S43959  
Ig mu chain V region (clone 13) - human (fragment)  
C;Species: Homo sapiens (man)

C;Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C;Accession: S43959  
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
Nucleic Acids Res. 22, 1389-1393, 1994  
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A;Reference number: S43956; MUID:94248036; PMID:8190629  
A;Accession: S43959  
A;Molecule type: DNA  
A;Residues: 1-4 <WAG>  
C;Keywords: immunoglobulin

Query Match 34.6%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 4  
S55238  
pallidipin - assassin bug (fragment)  
C;Species: Triatoma pallidipennis (assassin bug)  
C;Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
C;Accession: S55238  
R;Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin  
Biochem. J. 307, 465-470, 1995  
A;Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib  
A;Reference number: S55238; MUID:95251610; PMID:7733884  
A;Accession: S55238  
A;Molecule type: protein  
A;Residues: 1-4 <HAE>

Query Match 34.6%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 3 C 3

RESULT 5  
B22565  
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C;Accession: B22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: B22565  
A;Molecule type: protein  
A;Residues: 1-5 <KLO>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 6  
F22565  
R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C;Accession: F22565  
R;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: F22565  
A;Molecule type: protein  
A;Residues: 1-5 <KLO>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 3 C 3

RESULT 7  
A33882  
cadmium-binding pentapeptide - downy thornapple  
C;Species: Datura innoxia (downy thornapple)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993  
C;Accession: A33882  
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987  
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant ce  
A;Reference number: A94182; MUID:88016144; PMID:3477793  
A;Accession: A33882  
A;Molecule type: protein  
A;Residues: 1-5 <JAC>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 8  
B45525  
actin I - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C;Accession: B45525  
R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmake  
Mol. Biochem. Parasitol. 35, 167-176, 1989  
A;Title: Stage-specific expression and genomic organization of the actin genes of the mal  
A;Reference number: A45525; MUID:89364996; PMID:2671721  
A;Accession: B45525  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <WES>  
A;Cross-references: GB:J03988  
A;Note: the authors translated the codon GAA for residue 3 as Gly  
C;Comment: The actin I gene contains no introns.

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 4 C 4

RESULT 9  
S65726  
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)  
C;Species: Lumbricus terrestris (common earthworm)  
C;Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S65726  
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.



Biochim. Biophys. Acta 1292, 273-280, 1996  
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A;Reference number: S65721; MUID:96176855; PMID:8597573  
A;Accession: S65726  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <FUS>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 10  
JU0355  
lipopeptide WS1279 [validated] - Streptomyces willmorei  
C;Species: Streptomyces willmorei  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C;Accession: JU0355  
R;Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.  
Chem. Pharm. Bull. 39, 607-611, 1991  
A;Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial origin  
A;Reference number: JU0355; MUID:91300586; PMID:2070441  
A;Accession: JU0355  
A;Molecule type: protein  
A;Residues: 1-6 <TSU>  
A;Note: the structure was confirmed by synthesis  
C;Keywords: blocked amino end; lipoprotein  
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F;1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 1 C 1

RESULT 11  
C22565  
R-phycoerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C;Accession: C22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: C22565  
A;Molecule type: protein  
A;Residues: 1-6 <KLO>

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 12  
I37027  
protamine p1 - gorilla (fragment)  
C;Species: Gorilla gorilla (gorilla)  
C;Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jul-2000  
C;Accession: I37027

R;Queralt, R.; Oliva, R.  
Gene 133, 197-204, 1993  
A;Title: Identification of conserved potential regulatory sequences of the protamine-enc  
A;Reference number: I37013; MUID:94040810; PMID:8224908  
A;Accession: I37027  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: EMBL:Z12145; NID:G22910; PIDN:CAA78129.1; PID:G579612

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 6 C 6

RESULT 13  
I37263  
Y protein - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C;Accession: I37263  
R;Waeber, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternat  
A;Reference number: I37263; MUID:93010691; PMID:1396344  
A;Accession: I37263  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: EMBL:X68994; NID:G396171; PIDN:CAA48780.1; PID:G579816  
C;Genetics:  
A;Gene: CREB

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 4 C 4

RESULT 14  
H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fra  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C;Accession: H48394  
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A;Reference number: A48394; MUID:93250576; PMID:8485470  
A;Accession: H48394  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <MAT>  
A;Experimental source: milk  
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C;Keywords: Glycoprotein

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 6 C 6

RESULT 15  
I67345  
MHC H2-K-k cell surface glycoprotein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C;Accession: I67345  
R;Archibald, A.L.; Thompson, N.A.; Kvist, S.  
EMBO J. 5, 957-965, 1986  
A;Title: A single nucleotide difference at the 3' end of an intron causes differential splicing of the H2-Kb gene  
A;Reference number: I53243; MUID:86247587; PMID:3013627  
A;Accession: I67345  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458  
C;Genetics:  
A;Introns: 6/1  
C;Keywords: glycoprotein

Query Match	34.6%	Score 9;	DB 2;	Length 6;
Best Local Similarity	100.0%	Pred. No. 2.3e+05;		
Matches	1;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy	1	C	1
Db	4	C	4

Search completed: December 29, 2004, 21:42:53  
Job time : 20 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: December 29, 2004, 21:27:57 ; Search time 100 Seconds  
(without alignments)  
57.537 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	34.6	7	1 ASCL ALLAS	P84071 allium asca
2	9	34.6	7	1 BRHP CONIM	P58803 conus imper
3	9	34.6	7	2 Q9C5B3	Q9C5B3 arabidopsis
4	9	34.6	7	2 P70804	P70804 azotobacter
5	9	34.6	7	2 Q8GL12	Q8GL12 borrelia bu
6	9	34.6	7	2 Q55184	Q55184 rattus norv
7	9	34.6	7	2 Q66113	Q66113 cherry leaf
8	9	34.6	7	2 Q67113	Q67113 influenza a
9	9	34.6	7	2 Q9YIQ9	Q9YIQ9 human adeno
10	9	34.6	7	2 Q9YIR0	Q9YIR0 human adeno
11	9	34.6	7	2 Q9YVE3	Q9YVE3 human adeno
12	9	34.6	7	2 Q42564	Q42564 fugu rubrip
13	9	34.6	7	2 Q8JU20	Q8JJ20 gallus gall
14	9	34.6	8	1 ACT CARMA	P80709 carcinus ma
15	9	34.6	8	1 COW2 CONPU	P58785 conus purpu
16	9	34.6	8	1 GLUR HUMAN	P02729 homo sapien
17	9	34.6	8	2 Q6EGT1	Q6egt1 stemphylium
18	9	34.6	8	2 Q6EGV0	Q6egv0 stemphylium
19	9	34.6	8	2 Q6EGV2	Q6egv2 stemphylium
20	9	34.6	8	2 Q6EGV3	Q6egv3 stemphylium
21	9	34.6	8	2 Q6EGW2	Q6egw2 stemphylium
22	9	34.6	8	2 Q15888	Q15888 homo sapien
23	9	34.6	8	2 Q15890	Q15890 homo sapien
24	9	34.6	8	2 Q15900	Q15900 homo sapien
25	9	34.6	8	2 Q71UR9	Q71ur9 homo sapien
26	9	34.6	8	2 Q8IV87	Q8iv87 homo sapien
27	9	34.6	8	2 Q9Y4X6	Q9y4x6 homo sapien
28	9	34.6	8	2 Q9BY5	Q9byy5 homo sapien
29	9	34.6	8	2 Q7M3S2	Q7m3s2 trypanosoma
30	9	34.6	8	2 Q7M3S3	Q7m3s3 trypanosoma
31	9	34.6	8	2 Q7RBP6	Q7rbp6 plasmodium

32	9	34.6	8	2	Q7RC74	Q7rc74 plasmodium
33	9	34.6	8	2	Q02831	Q02831 oryctolagus
34	9	34.6	8	2	Q9TRY3	Q9try3 sus sp. ins
35	9	34.6	8	2	Q9BF82	Q9bf82 ursus arcto
36	9	34.6	8	2	Q9BF83	Q9bf83 canis famil
37	9	34.6	8	2	Q9BF84	Q9bf84 panthera on
38	9	34.6	8	2	Q9BF85	Q9bf85 leopardus p
39	9	34.6	8	2	Q9BF86	Q9bf86 felis silve
40	9	34.6	8	2	Q9BF87	Q9bf87 tapirus ind
41	9	34.6	8	2	Q9BF88	Q9bf88 equus cabal
42	9	34.6	8	2	Q9BF89	Q9bf89 okapia john
43	9	34.6	8	2	Q9BF90	Q9bf90 tragelaphus
44	9	34.6	8	2	Q9BF91	Q9bf91 hippopotamu
45	9	34.6	8	2	Q9BF92	Q9bf92 tursiops tr

ALIGNMENTS

RESULT 1  
ASCL\_ALLAS  
ID ASCL\_ALLAS STANDARD; PRT; 7 AA.  
AC P84071;  
DT 01-OCT-2004 (Rel. 45, Created)  
DT 01-OCT-2004 (Rel. 45, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Ascalin (Fragment).  
OS Allium ascalonicum (Shallot) (Allium cepa var. aggregatum).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
OC Allium.  
OX NCBI\_TaxID=28911;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Bulb;  
RX PubMed=12126728;  
RA Wang H.X., Ng T.B.;  
RT "Ascalin, a new anti-fungal peptide with human immunodeficiency virus  
type 1 reverse transcriptase-inhibiting activity from shallot bulbs.";  
RL Peptides 23:1025-1029(2002).  
CC -!- FUNCTION: Has antifungal activity against B.cinerea. Inhibits HIV-  
1 reverse transcriptase.  
CC -!- MISCELLANEOUS: Inhibits HIV-1 reverse transcriptase with an IC(50)  
of 10 uM.  
KW Direct protein sequencing; Fungicide.  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 712 MW; 687866D87EA6CB30 CRC64;

Query Match 34.6%; Score 9; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 3 C 3

RESULT 2  
BRHP\_CONIM  
ID BRHP\_CONIM STANDARD; PRT; 7 AA.  
AC P58803;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bromoheptapeptide Im.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;

RX MEDLINE=97184108; PubMed=9030520;  
RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,  
RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Oliveira B.M.,  
RA McIntosh J.M.;  
RT "A novel post-translational modification involving bromination of  
RT tryptophan. Identification of the residue, L-6-bromotryptophan, in  
RT peptides from *Conus imperialis* and *Conus radiatus* venom.";  
RL J. Biol. Chem. 272:4689-4698(1997).  
CC -I- FUNCTION: Does not elicit gross behavioral symptoms when injected  
CC centrally or peripherally in mice.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -I- MASS SPECTROMETRY: MW=853.19; METHOD=LSI; RANGE=1-7; NOTE=Ref.1.  
DR PIR: A58512; A58512.  
KW Amidation; Bromination; Direct protein sequencing;  
KW Pyrrolidone carboxylic acid.  
FT DISULFID 2 7  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 6 6 6'-bromotryptophan.  
FT MOD\_RES 7 7 Cysteine amide.  
SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;  
  
Query Match 34.6%; Score 9; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 2 C 2

RESULT 3

Q9C5B3  
ID Q9C5B3 PRELIMINARY; PRT; 7 AA.  
AC Q9C5B3;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein DiDi 10A-2b (Fragment).  
GN Name=DiDi 10A-2b;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Roots;  
RX MEDLINE=21171025; PubMed=11277426;  
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;  
RT "Arabidopsis thaliana genes expressed in the early compatible  
RT interaction with root-knot nematodes.";  
RL Mol. Plant Microbe Interact. 14:288-299(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Roots;  
RA Vercauteren I.J.R.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ286350; CAB71014.2; -.  
KW Hypothetical protein.  
FT NON\_TER 1 1  
FT NON\_TER 7 7  
SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;  
  
Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 3 C 3

RESULT 4  
P70804  
ID P70804 PRELIMINARY; PRT; 7 AA.  
AC P70804;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Algt protein (Fragment).  
GN Name=algt;  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E;  
RX MEDLINE=96427318; PubMed=8830682;  
RA Rehm B.H.A., Estesvag H., Valla S.;  
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is  
RT part of an alg gene cluster physically organized in a manner similar  
RT to that in *Pseudomonas aeruginosa*.";  
RL J. Bacteriol. 178:5884-5889(1996).  
DR EMBL; X87973; CAA61230.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;  
  
Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 1 C 1

RESULT 5

Q8GL12  
ID Q8GL12 PRELIMINARY; PRT; 7 AA.  
AC Q8GL12;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PF-50 protein (Fragment).  
GN Name=PF-50;  
OS *Borrelia burgdorferi* (Lyme disease spirochete).  
OG Plasmid group cp32-9.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N40;  
RX MEDLINE=22990544; PubMed=14629041;  
RA Stevenson B., Miller J.C.;  
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete  
RT erp genes generates sequence identity amidst diversity.";  
RL J. Mol. Evol. 57:309-324(2003).  
DR EMBL; AY142100; AAN17911.1; -.  
KW Plasmid.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 849 MW; 6337244330569ED0 CRC64;  
  
Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 1 C 1

RESULT 6

O55184  
ID O55184 PRELIMINARY; PRT; 7 AA.



AC O55184;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Orphan receptor TR4-NS (Fragment).  
GN Name=TR4;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=96198747; PubMed=8612486;  
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,  
RA Detera-Wadleigh S.D.;  
RT "Splice variants of rat TR4 orphan receptor: differential expression  
RT of novel sequences in the 5'-untranslated region and C-terminal  
RT domain.";  
RL Endocrinology 137:1562-1571(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=96299786; PubMed=8661150;  
RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;  
RT "New variants of the human and rat nuclear hormone receptor, TR4:  
RT expression and chromosomal localization of the human gene.";  
RL Genomics 35:361-366(1996).  
DR EMBL; U59454; AAB91433.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

RESULT 7  
Q66113  
ID Q66113 PRELIMINARY; PRT; 7 AA.  
AC Q66113;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE C-terminus of the viral replicase (Fragment).  
OS Cherry leaf roll virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
OC Nepovirus; Subgroup C.  
OX NCBI\_TaxID=12615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=walnut;  
RX MEDLINE=96124520; PubMed=8560786;  
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;  
RT "Long, nearly identical untranslated sequences at the 3' terminal  
RT regions of the genomic RNAs of cherry leafroll virus (walnut  
RT strain).";  
RL Virus Genes 10:245-252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=walnut;  
RX Borja M.;  
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.  
DR EMBL; Z34265; CAA84019.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 C 1  
|  
Db 4 C 4  
RESULT 8  
Q67113  
ID Q67113 PRELIMINARY; PRT; 7 AA.  
AC Q67113;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Influenza virus type A (Udorn/72) hemagglutinin (seg 4) cDNA, 3' end.  
DE (Fragment).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81001892; PubMed=7407922;  
RA Dhar R., Chanock R.M., Lai C.-J.;  
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza  
RT viral mRNA deduced from cloned complete genomic sequences.";  
RL Cell 21:495-500(1980).  
DR EMBL; M25045; AAA43202.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

RESULT 9  
Q9YIQ9  
ID Q9YIQ9 PRELIMINARY; PRT; 7 AA.  
AC Q9YIQ9;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pVI;  
OS Human adenovirus type 4.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=28280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Z-G T95-873;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute  
RT respiratory disease.";  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Z-G T95-873;  
RX Crawford-Miksza L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065064; AAD03659.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 6 C 6

RESULT 10

Q9YIRO Q9YIRO PRELIMINARY; PRT; 7 AA.  
AC Q9YIRO;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pVI;  
OS Human adenovirus type 7a.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;  
OC Human adenovirus type 7.  
OX NCBI\_TaxID=85755;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Kn T96-0620;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease.";  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Kn T96-0620;  
RA Crawford-Miksza L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065068; AAD03668.1; --  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 6 C 6

RESULT 11

Q9YVE3 Q9YVE3 PRELIMINARY; PRT; 7 AA.  
AC Q9YVE3;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pVI;  
OS Human adenovirus type 7.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=10519;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gomen;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease.";  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gomen;  
RA Crawford-Miksza L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065065; AAD03662.1; --  
FT NON\_TER 1

SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 6 C 6

RESULT 12

O42564 O42564 PRELIMINARY; PRT; 7 AA.  
AC O42564;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
GN Name=Scn8a;  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97442476; PubMed=9295353;  
RA Plummer N.W., McBurney M.W., Meisler M.H.;  
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";  
RL J. Biol. Chem. 272:24008-24015(1997).  
DR EMBL; U97673; AAB80916.1; --  
DR GO; GO:0005216; F:ion channel activity; IEA.  
KW Ionic channel.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 5 C 5

RESULT 13

Q8JJ20 Q8JJ20 PRELIMINARY; PRT; 7 AA.  
AC Q8JJ20;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Extracellular fatty acid binding protein (Fragment).  
GN Name=EXFABP;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Wang Q., Li N., Li H.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF487519; AAL96665.1; --  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 780 MW; 72CBIAB2D5BEBB70 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 14

ACT\_CARMA STANDARD; PRT; 8 AA.  
ID ACT\_CARMA  
AC P80709;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Actin (Fragment).  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
RA Baghdassarian D.;  
RT "A transaldolase. An enzyme implicated in crab steroidogenesis."  
RL Endocrine 5:23-32(1996).  
CC -!- FUNCTION: Actins are highly conserved proteins that are involved  
CC in various types of cell motility and are ubiquitously expressed  
CC in all eukaryotic cells.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:  
CC 6.8, its MW is: 46 kDa.  
CC -!- SIMILARITY: Belongs to the actin family.  
DR InterPro; IPR004001; Actin.  
DR InterPro; IPR004000; Actin\_like.  
DR PROSITE; PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE; PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE; PS01132; ACTINS\_ACT LIKE; PARTIAL.  
KW Direct protein sequencing; Structural protein.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;

Query Match 34.6%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 15

COW2\_CONPU STANDARD; PRT; 8 AA.  
ID COW2\_CONPU  
AC P58785;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE leu-contryphan-P.  
OS Conus purpurascens (Purple cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=41690;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC STRAIN=Clipperton Island; TISSUE=Venom;  
RX MEDLINE=99388839; PubMed=10461743;  
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
RA Olivera B.M.;  
RT "A novel D-leucine-containing Conus peptide: diverse conformational  
RT dynamics in the contryphan family.";

RL J. Pept. Res. 54:93-99(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSI; RANGE=1-8; NOTE=Ref.1.  
CC -!- SIMILARITY: Belongs to the contryphan family.  
KW D-amino acid; Direct protein sequencing; Hydroxylation; Toxin.  
FT DISULFID 2 8  
FT MOD\_RES 4 4 D-leucine.  
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;  
  
Query Match 34.6%; Score 9; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 C 1  
|  
Db 2 C 2  
  
Search completed: December 29, 2004, 21:41:51  
Job time : 102 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 69.6226 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	89	ADP30533	Adp30533 Human sec
2	18	69.2	89	ADP30531	Adp30531 Human sec
3	18	69.2	109	AAM93527	Aam93527 Human pol
4	18	69.2	109	ADL31230	Adl31230 Human pro
5	18	69.2	109	ADP30690	Adp30690 Human sec
6	18	69.2	144	ADP31474	Adp31474 Human sec
7	18	69.2	167	ABO69151	Abo69151 Pseudomon
8	18	69.2	171	ADP30794	Adp30794 Human sec
9	18	69.2	171	ADP30793	Adp30793 Human sec
10	18	69.2	183	ADP30806	Adp30806 Human sec
11	18	69.2	191	ABO76619	Abo76619 Pseudomon
12	18	69.2	228	ADP30921	Adp30921 Human sec
13	18	69.2	252	ADP31485	Adp31485 Human sec
14	18	69.2	258	ADP30479	Adp30479 Human sec
15	18	69.2	264	ADP31412	Adp31412 Human sec
16	18	69.2	270	ADP30500	Adp30500 Human sec
17	18	69.2	270	ADP31321	Adp31321 Human sec
18	18	69.2	294	ADP31473	Adp31473 Human sec
19	18	69.2	297	ADP31192	Adp31192 Human sec
20	18	69.2	328	AAM25285	Aam25285 Human pro
21	18	69.2	339	ADP30702	Adp30702 Human sec
22	18	69.2	348	ADP31441	Adp31441 Human sec
23	18	69.2	356	ABG21039	Abg21039 Novel hum
24	18	69.2	357	ADP31267	Adp31267 Human sec
25	18	69.2	357	ADP30505	Adp30505 Human sec

26	18	69.2	360	8	ADP31439	Adp31439 Human sec
27	18	69.2	390	8	ADP31218	Adp31218 Human sec
28	18	69.2	421	8	ADP31159	Adp31159 Human sec
29	18	69.2	426	8	ADP31495	Adp31495 Human sec
30	18	69.2	438	7	ABO82561	Abo82561 Pseudomon
31	18	69.2	453	8	ADP31465	Adp31465 Human sec
32	18	69.2	471	8	ADP30854	Adp30854 Human sec
33	18	69.2	525	8	ADP31227	Adp31227 Human sec
34	18	69.2	549	8	ADP30855	Adp30855 Human sec
35	18	69.2	555	8	ADP31416	Adp31416 Human sec
36	18	69.2	555	8	ADP31417	Adp31417 Human sec
37	18	69.2	588	8	ADP31699	Adp31699 Human sec
38	18	69.2	600	8	ADP30865	Adp30865 Human sec
39	18	69.2	604	8	ADP30940	Adp30940 Human sec
40	18	69.2	604	8	ADP30941	Adp30941 Human sec
41	18	69.2	605	8	ADP30507	Adp30507 Human sec
42	18	69.2	617	8	ADP31657	Adp31657 Human sec
43	18	69.2	626	6	ABR41596	Abr41596 Human DIT
44	18	69.2	645	8	ADP30858	Adp30858 Human sec
45	18	69.2	653	3	AAy94907	Aay94907 Human sec

ALIGNMENTS

RESULT 1  
ADP30533  
ID ADP30533 standard; protein; 89 AA.  
XX  
AC ADP30533;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #1300.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX



PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-041101P.  
PR 17-SEP-2002; 2002US-041111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX  
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
XX WPI; 2004-348438/32.  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 2531; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
SQ Sequence 89 AA;  
Query Match 69.2%; Score 18; DB 8; Length 89;  
Best Local Similarity 20.0%; Pred. No. 2.6;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 CXXXXXXXC 10  
|

Db 24 CTTAAAAAAC 33  
RESULT 2  
ADP30531  
ID ADP30531 standard; protein; 89 AA.  
XX  
AC ADP30531;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #1298.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
PR 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-041111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.



PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX  
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RP, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
DR WPI; 2004-348438/32.  
XX  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 2529; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOWEB and is not in the specification.  
XX  
SQ Sequence 89 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 89;  
Best Local Similarity 20.0%; Pred. No. 2.6;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXXC 10  
Db 24 CTTAAAAAAC 33  
  
RESULT 3  
AAM93527  
ID AAM93527 standard; protein; 109 AA.  
XX  
AC AAM93527;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide, SEQ ID NO: 3263.  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
XX  
OS Homo sapiens.  
XX  
PN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.

XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
DR WPI; 2001-524255/58.  
DR N-PSDB; AAK94457.  
XX  
PT 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX  
PS Claim 8; SEQ ID NO 3263; 1380pp + Sequence Listing; English.  
XX  
CC The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesising the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a polypeptide encoded by a full length  
CC human cDNA of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in CD-ROM  
CC format directly from EPO  
XX  
SQ Sequence 109 AA;  
  
Query Match 69.2%; Score 18; DB 4; Length 109;  
Best Local Similarity 20.0%; Pred. No. 2.7;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXXC 10  
Db 4 CSSSATSTSC 13  
  
RESULT 4  
ADL31230  
ID ADL31230 standard; protein; 109 AA.  
XX  
AC ADL31230;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human protein encoded by a full length cDNA clone seqID 3263.  
XX  
KW human; medicine; signal transduction; glycoprotein; transcription;  
KW oligo-capping method.  
XX  
OS Homo sapiens.  
XX  
PN EP1396543-A2.  
XX  
PD 10-MAR-2004.  
XX  
PF 07-JUL-2000; 2003EP-00025638.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX

DR WPI; 2004-204755/20.  
DR N-PSDB; ADL31229.  
XX  
PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
PT length human cDNAs.  
XX  
PS Example 1; SEQ ID NO 3263; 1340pp; English.  
XX  
CC This invention relates to a novel primers useful for synthesising full  
CC length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction,  
CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
CC ends using the oligo-capping method. This polypeptide sequence is a full  
CC length human protein of the invention.  
XX  
SQ Sequence 109 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 109;  
Best Local Similarity 20.0%; Pred. No. 2.7;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
Db 4 CSSSATSTSC 13  
  
RESULT 5  
ADP30690  
ID ADP30690 standard; protein; 109 AA.  
XX  
AC ADP30690;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #1457.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
PR 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.

PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX  
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
DR WPI; 2004-348438/32.  
XX  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 2688; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytosstatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPoWEB and is not in the specification.  
XX  
SQ Sequence 109 AA;

Query Match 69.2%; Score 18; DB 8; Length 109;  
Best Local Similarity 20.0%; Pred. No. 2.7;

Matches	2;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;
Qy	1	CXXXXXXXXC 10							
Db	96	CTTTTATATC 105							
RESULT 6									
ADP31474									
ID	ADP31474 standard; protein; 144 AA.								
XX									
AC	ADP31474;								
XX									
DT	12-AUG-2004 (first entry)								
XX									
DE	Human secreted protein SEQ ID #2241.								
XX									
KW	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;								
KW	cancer; inflammatory; immune; human secreted protein.								
XX									
OS	Homo sapiens.								
XX									
PN	WO2004035732-A2.								
XX									
PD	29-APR-2004.								
XX									
PF	28-AUG-2003; 2003WO-US026780.								
XX									
PR	29-AUG-2002; 2002US-0406576P.								
PR	29-AUG-2002; 2002US-0406579P.								
PR	29-AUG-2002; 2002US-0406585P.								
PR	29-AUG-2002; 2002US-0406588P.								
PR	29-AUG-2002; 2002US-0406608P.								
PR	29-AUG-2002; 2002US-0406611P.								
PR	29-AUG-2002; 2002US-0406612P.								
PR	29-AUG-2002; 2002US-0406616P.								
PR	29-AUG-2002; 2002US-0406640P.								
PR	29-AUG-2002; 2002US-0406642P.								
PR	29-AUG-2002; 2002US-0406646P.								
PR	29-AUG-2002; 2002US-0406653P.								
PR	29-AUG-2002; 2002US-0406655P.								
PR	29-AUG-2002; 2002US-0406666P.								
PR	17-SEP-2002; 2002US-0410946P.								
PR	17-SEP-2002; 2002US-0410947P.								
PR	17-SEP-2002; 2002US-0410948P.								
PR	17-SEP-2002; 2002US-0410949P.								
PR	17-SEP-2002; 2002US-0410953P.								
PR	17-SEP-2002; 2002US-0410957P.								
PR	17-SEP-2002; 2002US-0410958P.								
PR	17-SEP-2002; 2002US-0410959P.								
PR	17-SEP-2002; 2002US-0410960P.								
PR	17-SEP-2002; 2002US-0410961P.								
PR	17-SEP-2002; 2002US-0410962P.								
PR	17-SEP-2002; 2002US-0411019P.								
PR	17-SEP-2002; 2002US-0411022P.								
PR	17-SEP-2002; 2002US-0411023P.								
PR	17-SEP-2002; 2002US-0411024P.								
PR	17-SEP-2002; 2002US-0411032P.								
PR	17-SEP-2002; 2002US-0411035P.								
PR	17-SEP-2002; 2002US-0411037P.								
PR	17-SEP-2002; 2002US-0411041P.								
PR	17-SEP-2002; 2002US-0411045P.								
PR	17-SEP-2002; 2002US-0411046P.								
PR	17-SEP-2002; 2002US-0411048P.								
PR	17-SEP-2002; 2002US-0411052P.								
PR	17-SEP-2002; 2002US-0411055P.								
PR	17-SEP-2002; 2002US-0411073P.								
PR	17-SEP-2002; 2002US-0411082P.								
PR	17-SEP-2002; 2002US-0411101P.								
PR	17-SEP-2002; 2002US-0411111P.								
PR	18-APR-2003; 2003US-0463700P.								
PR	18-APR-2003; 2003US-0463708P.								
PR	18-APR-2003; 2003US-0463716P.								

PR	18-APR-2003; 2003US-0463732P.
PR	02-MAY-2003; 2003US-0467199P.
PR	02-MAY-2003; 2003US-0467201P.
PR	02-MAY-2003; 2003US-0467203P.
PR	02-MAY-2003; 2003US-0467230P.
PR	19-MAY-2003; 2003US-0471306P.
PR	19-MAY-2003; 2003US-0471336P.
PR	22-MAY-2003; 2003US-0472420P.
PR	22-MAY-2003; 2003US-0472430P.
PR	09-JUN-2003; 2003US-0476609P.
PR	09-JUN-2003; 2003US-0476641P.
PR	08-JUL-2003; 2003US-0485218P.
PR	08-JUL-2003; 2003US-0485223P.
PR	08-JUL-2003; 2003US-0485224P.
PR	08-JUL-2003; 2003US-0485325P.
PR	14-JUL-2003; 2003US-0486446P.
PR	14-JUL-2003; 2003US-0486480P.
PR	15-JUL-2003; 2003US-0486891P.
PR	15-JUL-2003; 2003US-0486960P.
PR	08-AUG-2003; 2003US-0493341P.
PR	08-AUG-2003; 2003US-0493370P.
PR	08-AUG-2003; 2003US-0493573P.
PR	08-AUG-2003; 2003US-0493577P.
XX	
PA	(FIVE-) FIVE PRIME THERAPEUTICS INC.
XX	
PI	Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI	Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI	Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX	
DR	WPI; 2004-348438/32.
XX	
PT	New nucleic acid molecule for diagnosing, preventing or treating diseases
PT	such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT	genetic, bacterial and viral diseases.
XX	
PS	Claim 1; SEQ ID NO 3472; 428pp; English.
XX	
CC	The present invention relates to an isolated nucleic acid molecule
CC	encoding a polypeptide which is believed to be cytostatic,
CC	antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC	composition and methods are useful for diagnosing, preventing and
CC	treating diseases such as proliferative (e.g. cancer), inflammatory,
CC	immune, metabolic, genetic, bacterial and viral diseases. The present
CC	sequence represents a human secreted protein. The present sequence is
CC	available on WIPOWEB and is not in the specification.
XX	
SQ	Sequence 144 AA;

Query Match	69.2%;	Score 18;	DB 8;	Length 144;
Best Local Similarity	20.0%;	Pred. No. 2.8;		
Matches	2;	Conservative	0;	Mismatches 8;
Indels	0;	Gaps	0;	

Qy	1	CXXXXXXXXXC 10
Db	72	CAATAAAATC 81

RESULT 7	
ABO69151	
ID	ABO69151 standard; protein; 167 AA.
XX	
AC	ABO69151;
XX	
DT	29-JUL-2004 (first entry)
XX	
DE	Pseudomonas aeruginosa polypeptide #1326.
XX	
KW	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX	
OS	Pseudomonas aeruginosa.
XX	
PN	US6551795-B1.

XX 22-APR-2003.  
PD 18-FEB-1999; 99US-00252991.  
XX 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
PI WPI; 2003-615309/58.  
DR N-PSDB; ABD02722.  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX Disclosure; SEQ ID NO 17897; 455pp; English.  
PS The invention relates to Pseudomonas aeruginosa polypeptides and the  
XX polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX Sequence 167 AA;  
SQ Query Match 69.2%; Score 18; DB 7; Length 167;  
Best Local Similarity 20.0%; Pred. No. 2.9;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 1 CXXXXXXXXC 10  
Db 60 CSTSTSTTSC 69  
RESULT 8  
ADP30794  
ID ADP30794 standard; protein; 171 AA.  
XX ADP30794;  
AC ADP30794;  
XX 12-AUG-2004 (first entry)  
DT Human secreted protein SEQ ID #1561.  
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
KW Homo sapiens.  
XX WO2004035732-A2.  
OS  
XX 29-APR-2004.  
PD 28-AUG-2003; 2003WO-US026780.  
XX 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR

PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 22-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
DR



XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 2792; 428pp; English.  
XX

CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOWEB and is not in the specification.  
XX  
SQ Sequence 171 AA;

Query Match 69.2%; Score 18; DB 8; Length 171;  
Best Local Similarity 20.0%; Pred. No. 2.9;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
| |  
Db 146 CAAATAAAC 155

RESULT 9  
ADP30793  
ID ADP30793 standard; protein; 171 AA.

XX ADP30793;  
AC  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #1560.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.

PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
PR 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.

PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

WPI; 2004-348438/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases  
such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
genetic, bacterial and viral diseases.

Claim 1; SEQ ID NO 2791; 428pp; English.

The present invention relates to an isolated nucleic acid molecule  
encoding a polypeptide which is believed to be cytostatic,  
antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
composition and methods are useful for diagnosing, preventing and  
treating diseases such as proliferative (e.g. cancer), inflammatory,  
immune, metabolic, genetic, bacterial and viral diseases. The present  
sequence represents a human secreted protein. The present sequence is  
available on WIPOWEB and is not in the specification.

Sequence 171 AA;

Query Match 69.2%; Score 18; DB 8; Length 171;  
Best Local Similarity 20.0%; Pred. No. 2.9;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;





XX 18-FEB-1999; 99US-00252991.  
PF 18-FEB-1998; 98US-0074788P.  
XX 27-JUL-1998; 98US-0094190P.  
PR (GENO-) GENOME THERAPEUTICS CORP.  
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.  
PI N-PSDB; ABD10190.  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX Disclosure; SEQ ID NO 25365; 455pp; English.  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 191 AA;  
  
Query Match 69.2%; Score 18; DB 7; Length 191;  
Best Local Similarity 20.0%; Pred. No. 3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXXC 10  
Db 49 CSTAASATSC 58  
  
RESULT 12  
ADP30921  
ID ADP30921 standard; protein; 228 AA.  
XX  
AC ADP30921;  
XX 12-AUG-2004 (first entry)  
XX Human secreted protein SEQ ID #1688.  
DE  
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
KW Homo sapiens.  
OS  
XX WO2004035732-A2.  
PN  
XX 29-APR-2004.  
PD  
XX 28-AUG-2003; 2003WO-US026780.  
PF  
XX 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
XX Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT

PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 2919; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
SQ Sequence 228 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 228;  
Best Local Similarity 20.0%; Pred. No. 3.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
Db 54 CATAAATTAC 63  
  
RESULT 13  
ADP31485  
ID ADP31485 standard; protein; 252 AA.  
XX  
AC ADP31485;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #2252.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
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PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
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PR 08-AUG-2003; 2003US-0493577P.  
XX  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX  
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
DR WPI; 2004-348438/32.  
XX  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 3483; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
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Best Local Similarity 20.0%; Pred. No. 3.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
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DT	12-AUG-2004 (first entry)	
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DE	Human secreted protein SEQ ID #1246.	
XX		
KW	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;	
KW	cancer; inflammatory; immune; human secreted protein.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004035732-A2.	
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PD	29-APR-2004.	
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PF	28-AUG-2003; 2003WO-US026780.	
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PR	17-SEP-2002; 2002US-0411052P.	
PR	17-SEP-2002; 2002US-0411055P.	
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PR	18-APR-2003; 2003US-0463700P.	
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PR	02-MAY-2003; 2003US-0467199P.	
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PR	02-MAY-2003; 2003US-0467203P.	

PR	02-MAY-2003; 2003US-0467230P.	
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PR	09-JUN-2003; 2003US-0476609P.	
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PR	08-JUL-2003; 2003US-0485218P.	
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XX		
PA	(FIVE-) FIVE PRIME THERAPEUTICS INC.	
XX		
PI	Williams LT, Chu K, Lee E, Hestir K, Beurang PA, Behrens D;	
PI	Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;	
PI	Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;	
XX		
DR	WPI; 2004-348438/32.	
XX		
PT	New nucleic acid molecule for diagnosing, preventing or treating diseases	
PT	such as proliferative (e.g. cancer), inflammatory, immune, metabolic,	
PT	genetic, bacterial and viral diseases.	
XX		
PS	Claim 1; SEQ ID NO 2477; 428pp; English.	
XX		
CC	The present invention relates to an isolated nucleic acid molecule	
CC	encoding a polypeptide which is believed to be cytostatic,	
CC	antiinflammatory, immunosuppressive, antibacterial and virucidal. The	
CC	composition and methods are useful for diagnosing, preventing and	
CC	treating diseases such as proliferative (e.g. cancer), inflammatory,	
CC	immune, metabolic, genetic, bacterial and viral diseases. The present	
CC	sequence represents a human secreted protein. The present sequence is	
CC	available on WIPOWEB and is not in the specification.	
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SQ	Sequence 258 AA;	
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Best Local Similarity 20.0%; Pred. No. 3.2;		
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;		
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DT	12-AUG-2004 (first entry)	
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DE	Human secreted protein SEQ ID #2179.	
XX		
KW	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;	
KW	cancer; inflammatory; immune; human secreted protein.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004035732-A2.	
XX		
PD	29-APR-2004.	
XX		

PF 28-AUG-2003; 2003WO-US026780.  
XX 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
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PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
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PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
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PR 22-MAY-2003; 2003US-0472420P.  
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PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
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PR 14-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
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(FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX  
XX

PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
DR WPI; 2004-348438/32.  
XX  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 3410; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOWEB and is not in the specification.  
XX  
SQ Sequence 264 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 264;  
Best Local Similarity 20.0%; Pred. No. 3.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
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Db 186 CATAAAATTC 195

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Job time : 71.6226 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 23.0189 Seconds  
(without alignments)  
28.810 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	69.2	167	4	US-09-252-991A-17897 Sequence 17897, A
3	18	69.2	191	4	US-09-252-991A-25365 Sequence 25365, A
4	18	69.2	438	4	US-09-252-991A-31307 Sequence 31307, A
5	18	69.2	777	4	US-09-270-767-44409 Sequence 44409, A
6	18	69.2	801	1	US-07-906-349A-6 Sequence 6, Appli
7	18	69.2	1388	4	US-09-463-048A-6 Sequence 6, Appli
8	18	69.2	1497	4	US-09-060-854B-2 Sequence 2, Appli
9	18	69.2	1917	4	US-09-627-650B-5 Sequence 5, Appli
10	18	69.2	1917	4	US-09-436-063C-5 Sequence 5, Appli
11	17	65.4	45	2	US-08-824-379-3 Sequence 3, Appli
12	17	65.4	48	5	PCT-US96-01720-9 Sequence 9, Appli
13	17	65.4	150	4	US-09-252-991A-31728 Sequence 31728, A
14	17	65.4	156	4	US-09-252-991A-20612 Sequence 20612, A
15	17	65.4	169	4	US-09-252-991A-20344 Sequence 20344, A
16	17	65.4	169	4	US-09-252-991A-24301 Sequence 24301, A
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18	17	65.4	191	4	US-09-252-991A-19331 Sequence 19331, A
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22	17	65.4	229	4	US-09-252-991A-29247 Sequence 29247, A
23	17	65.4	243	4	US-09-252-991A-25814 Sequence 25814, A
24	17	65.4	281	4	US-09-252-991A-29199 Sequence 29199, A
25	17	65.4	314	4	US-09-252-991A-31368 Sequence 31368, A
26	17	65.4	341	2	US-08-209-521-11 Sequence 11, Appl
27	17	65.4	414	4	US-09-252-991A-25096 Sequence 25096, A

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29	17	65.4	1076	4	US-10-140-002-219 Sequence 219, App
30	17	65.4	1400	3	US-08-630-915A-37 Sequence 37, Appl
31	17	65.4	1400	4	US-09-879-957-37 Sequence 37, Appl
32	17	65.4	1461	4	US-10-142-231-86 Sequence 86, Appl
33	17	65.4	1652	4	US-09-627-650B-1 Sequence 1, Appli
34	17	65.4	1652	4	US-09-436-063C-1 Sequence 1, Appli
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37	17	65.4	2544	4	US-09-627-650B-3 Sequence 3, Appli
38	17	65.4	2544	4	US-09-436-063C-3 Sequence 3, Appli
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40	17	65.4	2601	4	US-09-436-063C-9 Sequence 9, Appli
41	17	65.4	2732	4	US-09-086-436-30 Sequence 30, Appl
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43	16	61.5	20	4	US-09-419-381-115 Sequence 115, App
44	16	61.5	24	3	US-08-482-085B-92 Sequence 92, Appl
45	16	61.5	24	3	US-08-900-230-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1  
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; Patent No. 5919638  
; GENERAL INFORMATION:  
; APPLICANT: Russell, John C.  
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Abbott Laboratories  
; STREET: 100 Abbott Park Road D377/AP6D  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/727,688  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Foremski, Priscilla E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5967.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (847) 937-0378  
; TELEFAX: (847) 938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 5919638e  
US-08-727-688-23

Query Match 69.2%; Score 18; DB 2; Length 14;  
Best Local Similarity 20.0%; Pred. No. 0.17;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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Db 3 CSSSSSSSSAC 12

RESULT 2

US-09-252-991A-17897

; Sequence 17897, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 17897

; LENGTH: 167

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-17897

Query Match 69.2%; Score 18; DB 4; Length 167;

Best Local Similarity 20.0%; Pred. No. 0.28;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 60 CSTSTSTTSC 69

RESULT 3

US-09-252-991A-25365

; Sequence 25365, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 25365

; LENGTH: 191

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25365

Query Match 69.2%; Score 18; DB 4; Length 191;

Best Local Similarity 20.0%; Pred. No. 0.29;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 49 CSTAASATSC 58

RESULT 4

US-09-252-991A-31307

; Sequence 31307, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 31307

; LENGTH: 438

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31307

Query Match 69.2%; Score 18; DB 4; Length 438;

Best Local Similarity 20.0%; Pred. No. 0.34;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 56 CSAATASSTC 65

RESULT 5

US-09-270-767-44409

; Sequence 44409, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 44409

; LENGTH: 777

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-44409

Query Match 69.2%; Score 18; DB 4; Length 777;

Best Local Similarity 20.0%; Pred. No. 0.39;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 729 CSTSSSSSSC 738

RESULT 6

US-07-906-349A-6

; Sequence 6, Application US/07906349A

; Patent No. 5434064

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph

; APPLICANT: Skolnik, Edward Y.

; APPLICANT: Margolis, Benjamin L.

; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND

; TITLE OF INVENTION: TARGET PROTEINS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM: Floppy disk

; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,349A
; FILING DATE: 30-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/643,237
; FILING DATE: 18-JAN-1991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 801 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-906-349A-6

Query Match      69.2%; Score 18; DB 1; Length 801;
Best Local Similarity 20.0%; Pred. No. 0.39;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      608 CTTTTRTTTC 617

RESULT 7
US-09-463-048A-6
; Sequence 6, Application US/09463048A
; Patent No. 6630619
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photobacterium
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/09/463,048A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
; US-09-463-048A-6

Query Match      69.2%; Score 18; DB 4; Length 1388;
Best Local Similarity 20.0%; Pred. No. 0.43;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      8 CTAATAATTC 17

RESULT 8
US-09-060-854B-2
; Sequence 2, Application US/09060854B
; Patent No. 6642011
; GENERAL INFORMATION:
; APPLICANT: Estell, David Aaron
; TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
; TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011-H
; TITLE OF INVENTION: Proteins
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; FILE REFERENCE: GC532
; CURRENT APPLICATION NUMBER: US/09/060,854B
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
; US-09-060-854B-2

Query Match      69.2%; Score 18; DB 4; Length 1497;
Best Local Similarity 20.0%; Pred. No. 0.44;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      30 CAATTAATAC 39

RESULT 9
US-09-627-650B-5
; Sequence 5, Application US/09627650B
; Patent No. 6406872
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 21101.0009U3
; CURRENT APPLICATION NUMBER: US/09/627,650B
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/436,063
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107,727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-627-650B-5

Query Match      69.2%; Score 18; DB 4; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.46;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      1049 CAAATATATC 1058

RESULT 10
US-09-436-063C-5
; Sequence 5, Application US/09436063C
; Patent No. 6407210
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: P-1095corrected
; CURRENT APPLICATION NUMBER: US/09/436,063C
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
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US-09-436-063C-5
Query Match          69.2%; Score 18; DB 4; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.46;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1049 CAAATATATC 1058

RESULT 11
US-08-824-379-3
; Sequence 3, Application US/08824379
; Patent No. 5885801
; GENERAL INFORMATION:
; APPLICANT: Rao, A. Gururaj
; TITLE OF INVENTION: High Threonine Derivatives of
; TITLE OF INVENTION: Alpha-Hordothionin
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States of America
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,379
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/459,180
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Simon, Soma G.
; REGISTRATION NUMBER: 37,444
; REFERENCE/DOCKET NUMBER: 354-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-248-4896
; TELEFAX: 515-248-4844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-824-379-3
Query Match          65.4%; Score 17; DB 2; Length 45;
Best Local Similarity 20.0%; Pred. No. 0.99;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 16 CTTTATTTC 25

RESULT 12
PCT-US96-01720-9
; Sequence 9, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01720-9
Query Match          65.4%; Score 17; DB 5; Length 48;
Best Local Similarity 20.0%; Pred. No. 1;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 3 CGTTTAAATC 12

RESULT 13
US-09-252-991A-31728
; Sequence 31728, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31728
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31728
Query Match          65.4%; Score 17; DB 4; Length 150;
Best Local Similarity 20.0%; Pred. No. 1.3;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 35 CASAAAISSC 44

RESULT 14
US-09-252-991A-20612
; Sequence 20612, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20612  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20612

Query Match 65.4%; Score 17; DB 4; Length 156;  
Best Local Similarity 20.0%; Pred. No. 1.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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Db 78 CSTTAGSTSC 87

RESULT 15

US-09-252-991A-20344  
; Sequence 20344, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20344  
; LENGTH: 169  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20344

Query Match 65.4%; Score 17; DB 4; Length 169;  
Best Local Similarity 20.0%; Pred. No. 1.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 17 CSTSSARATC 26

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GenCore version 5.1.6  
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Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10  
Scoring table: BLOSUM62  
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Searched: 1599051 seqs, 359727711 residues  
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Minimum DB seq length: 0  
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Listing first 45 summaries

Database : Published Applications AA:\*  
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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
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13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	33	16 US-10-697-399-10	Sequence 10, Appl
2	18	69.2	37	16 US-10-380-927-7	Sequence 7, Appli
3	18	69.2	328	15 US-10-296-115-800	Sequence 800, App
4	18	69.2	429	15 US-10-424-955A-28	Sequence 28, Appl
5	18	69.2	598	16 US-10-437-963-162631	Sequence 162631,
6	18	69.2	630	10 US-09-791-279-86	Sequence 86, Appl
7	18	69.2	647	14 US-10-184-644-539	Sequence 539, App
8	18	69.2	647	14 US-10-184-634-539	Sequence 539, App
9	18	69.2	653	10 US-09-374-046A-20	Sequence 20, Appl
10	18	69.2	653	14 US-10-102-524-1851	Sequence 1851, Ap
11	18	69.2	653	14 US-10-331-496A-81	Sequence 81, Appl
12	18	69.2	653	15 US-10-616-263-20	Sequence 20, Appl
13	18	69.2	693	14 US-10-123-155-499	Sequence 499, App

14	18	69.2	693	14	US-10-146-731-499	Sequence 499, App
15	18	69.2	693	14	US-10-140-472-499	Sequence 499, App
16	18	69.2	693	14	US-10-141-761-499	Sequence 499, App
17	18	69.2	693	14	US-10-142-885-499	Sequence 499, App
18	18	69.2	693	14	US-10-158-790-499	Sequence 499, App
19	18	69.2	693	14	US-10-137-871-499	Sequence 499, App
20	18	69.2	693	14	US-10-140-923-499	Sequence 499, App
21	18	69.2	693	14	US-10-141-756-499	Sequence 499, App
22	18	69.2	693	14	US-10-141-759-499	Sequence 499, App
23	18	69.2	693	14	US-10-140-805-499	Sequence 499, App
24	18	69.2	693	14	US-10-140-864-499	Sequence 499, App
25	18	69.2	693	15	US-10-142-426-499	Sequence 129702,
26	18	69.2	733	16	US-10-437-963-129702	Sequence 167, App
27	18	69.2	735	14	US-10-184-644-167	Sequence 167, App
28	18	69.2	735	14	US-10-184-634-167	Sequence 153, App
29	18	69.2	755	14	US-10-123-155-153	Sequence 153, App
30	18	69.2	755	14	US-10-146-731-153	Sequence 153, App
31	18	69.2	755	14	US-10-140-472-153	Sequence 153, App
32	18	69.2	755	14	US-10-141-761-153	Sequence 153, App
33	18	69.2	755	14	US-10-142-885-153	Sequence 153, App
34	18	69.2	755	14	US-10-158-790-153	Sequence 153, App
35	18	69.2	755	14	US-10-137-871-153	Sequence 153, App
36	18	69.2	755	14	US-10-140-923-153	Sequence 153, App
37	18	69.2	755	14	US-10-141-756-153	Sequence 153, App
38	18	69.2	755	14	US-10-141-759-153	Sequence 153, App
39	18	69.2	755	14	US-10-140-805-153	Sequence 153, App
40	18	69.2	755	14	US-10-140-864-153	Sequence 153, App
41	18	69.2	755	15	US-10-142-426-153	Sequence 379, App
42	18	69.2	823	14	US-10-123-155-379	Sequence 379, App
43	18	69.2	823	14	US-10-146-731-379	Sequence 379, App
44	18	69.2	823	14	US-10-140-472-379	Sequence 379, App
45	18	69.2	823	14	US-10-141-761-379	Sequence 379, App

ALIGNMENTS

RESULT 1  
US-10-697-399-10  
; Sequence 10, Application US/10697399  
; Publication No. US20040162413A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Vasserot, Alain P.  
; APPLICANT: Marquis, David P.  
; APPLICANT: Smith, Eric P.  
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity  
; FILE REFERENCE: AME-08122  
; CURRENT APPLICATION NUMBER: US/10/697,399  
; CURRENT FILING DATE: 2003-10-30  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-697-399-10

Query Match 69.2%; Score 18; DB 16; Length 33;  
Best Local Similarity 20.0%; Pred. No. 2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
|  
Db 24 CTATTAAAC 33

RESULT 2  
US-10-380-927-7  
; Sequence 7, Application US/10380927

; Publication No. US20040110165A1  
; GENERAL INFORMATION:  
; APPLICANT: Larry W. Kwak  
; APPLICANT: Arya Biragyn  
; TITLE OF INVENTION: VIRAL CHEMOKINE-ANTIGEN FUSION PROTEINS  
; FILE REFERENCE: 14014.0381U2  
; CURRENT APPLICATION NUMBER: US/10/380,927  
; CURRENT FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: PCT/US01/29075  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: 60/233,067  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence = Note  
; OTHER INFORMATION: Synthetic Construct  
US-10-380-927-7

Query Match 69.2%; Score 18; DB 16; Length 37;  
Best Local Similarity 20.0%; Pred. No. 2.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 7 CTTTATTTC 16

RESULT 3  
US-10-296-115-800  
; Sequence 800, Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 800  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(328)  
; OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3  
US-10-296-115-800

Query Match 69.2%; Score 18; DB 15; Length 328;  
Best Local Similarity 20.0%; Pred. No. 3.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 63 CAAAAAAAC 72

RESULT 4  
US-10-424-955A-28  
; Sequence 28, Application US/10424955A  
; Publication No. US20040014658A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCHON BIOTECH LTD  
; APPLICANT: Bogin, Oren

; APPLICANT: Yayon, Avner  
; APPLICANT: Adar, Rivka  
; TITLE OF INVENTION: ACTIVE VARIANTS OF EGF WITH IMPROVED SPECIFICITY  
; FILE REFERENCE: 139380 IL  
; CURRENT APPLICATION NUMBER: US/10/424,955A  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: 139380 IL  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-424-955A-28

Query Match 69.2%; Score 18; DB 15; Length 429;  
Best Local Similarity 20.0%; Pred. No. 3.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 397 CATTTTATAC 406

RESULT 5  
US-10-437-963-162631  
; Sequence 162631, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 162631  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_61704C.1.pep  
US-10-437-963-162631

Query Match 69.2%; Score 18; DB 16; Length 598;  
Best Local Similarity 20.0%; Pred. No. 3.4;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 148 CTASSSSSC 157

RESULT 6  
US-09-791-279-86  
; Sequence 86, Application US/09791279  
; Publication No. US20030050456A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis  
; APPLICANT: Lind, Peter  
; TITLE OF INVENTION: No. US20030050456A1el G Protein-Coupled Receptors  
; FILE REFERENCE: 00048.US1  
; CURRENT APPLICATION NUMBER: US/09/791,279

;  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,715  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184725  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,712  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,606  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,602  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,604  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,822  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,710  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,689  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,690  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,716  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 86  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-279-86

Query Match 69.2%; Score 18; DB 10; Length 630;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
DB 128 CTTTTTTAAAC 137

RESULT 7  
US-10-184-644-539  
; Sequence 539, Application US/10184644  
; Publication No. US2003004930A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C227  
; CURRENT APPLICATION NUMBER: US/10/184,644  
; CURRENT FILING DATE: 2002-06-28  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 539  
; LENGTH: 647  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-184-644-539

Query Match 69.2%; Score 18; DB 14; Length 647;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
DB 288 CTTAAAAAAC 297  
RESULT 8  
US-10-184-634-539  
; Sequence 539, Application US/10184634  
; Publication No. US20030068684A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C217  
; CURRENT APPLICATION NUMBER: US/10/184,634  
; CURRENT FILING DATE: 2002-06-28  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 539  
; LENGTH: 647  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-184-634-539

Query Match 69.2%; Score 18; DB 14; Length 647;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
DB 288 CTTAAAAAAC 297

RESULT 9  
US-09-374-046A-20  
; Sequence 20, Application US/09374046A  
; Publication No. US20030096951A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steininger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fecht, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: GI 6075-83A  
; CURRENT APPLICATION NUMBER: US/09/374,046A  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 240  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 653  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: UNSURE  
; LOCATION: (114)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (247)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (290)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (601)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (604)  
US-09-374-046A-20

Query Match 69.2%; Score 18; DB 10; Length 653;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
|  
Db 173 CAAAAAAAAC 182

RESULT 10  
US-10-102-524-1851  
; Sequence 1851, Application US/10102524  
; Publication No. US20030109434A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Gordon, Brian  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.572  
; CURRENT APPLICATION NUMBER: US/10/102,524  
; CURRENT FILING DATE: 2002-03-19  
; NUMBER OF SEQ ID NOS: 1863  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1851  
; LENGTH: 653  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variant  
; LOCATION: 114,247,290,601,604  
; OTHER INFORMATION: Xaa = Any amino acid  
US-10-102-524-1851

Query Match 69.2%; Score 18; DB 14; Length 653;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
|  
Db 173 CAAAAAAAAC 182

RESULT 11  
US-10-331-496A-81  
; Sequence 81, Application US/10331496A  
; Publication No. US20030228305A1  
; GENERAL INFORMATION:  
; APPLICANT: FRANTZ,GRETCHEN  
; APPLICANT: HILLAN,KENNETH J.  
; APPLICANT: PHILLIPS,HEIDI S.  
; APPLICANT: POLAKIS,PAUL  
; APPLICANT: SMITH,VICTORIA  
; APPLICANT: SPENCER,SUSAN D.  
; APPLICANT: WILLIAMS,P. MICKEY

; APPLICANT: WU,THOMAS D.  
; APPLICANT: ZHANG,ZEMIN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; FILE REFERENCE: P5014R1-PCT  
; CURRENT APPLICATION NUMBER: US/10/331,496A  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 60/345,444  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US 60/351,885  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/360,066  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: US 60/362,004  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/366,869  
; PRIOR FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,284  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: US 60/368,679  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645  
; PRIOR FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 81  
; LENGTH: 653  
; TYPE: PRT  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: X  
; LOCATION: 114, 247, 290, 601, 604  
; OTHER INFORMATION: Unknown base  
US-10-331-496A-81

Query Match 69.2%; Score 18; DB 14; Length 653;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
|  
Db 173 CAAAAAAAAC 182

RESULT 12  
US-10-616-263-20  
; Sequence 20, Application US/10616263  
; Publication No. US20040038276A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: Lavallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steiningger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 00766.000103.5  
; CURRENT APPLICATION NUMBER: US/10/616,263  
; CURRENT FILING DATE: 2003-07-08  
; NUMBER OF SEQ ID NOS: 240  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 653  
; TYPE: PRT



; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (114)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (247)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (290)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (601)  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (604)  
US-10-616-263-20

Query Match 69.2%; Score 18; DB 15; Length 653;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 173 CAAAAAAC 182

RESULT 13

US-10-123-155-499  
; Sequence 499, Application US/10123155  
; Publication No. US20030068794A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C30  
; CURRENT APPLICATION NUMBER: US/10/123,155  
; CURRENT FILING DATE: 2002-04-15  
; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 499  
; LENGTH: 693  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-123-155-499

Query Match 69.2%; Score 18; DB 14; Length 693;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 613 CAATAAAATC 622

RESULT 14

US-10-146-731-499

; Sequence 499, Application US/10146731  
; Publication No. US20030129692A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C323  
; CURRENT APPLICATION NUMBER: US/10/146,731  
; CURRENT FILING DATE: 2002-05-15  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 499  
; LENGTH: 693  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-146-731-499

Query Match 69.2%; Score 18; DB 14; Length 693;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 613 CAATAAAATC 622

RESULT 15

US-10-140-472-499  
; Sequence 499, Application US/10140472  
; Publication No. US20030138888A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C168  
; CURRENT APPLICATION NUMBER: US/10/140,472  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 499  
; LENGTH: 693



```
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-472-499

Query Match      69.2%; Score 18; DB 14; Length 693;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
      |
Db      613 CAATAAAATC 622
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Search completed: December 30, 2004, 13:49:59  
Job time : 75.5283 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	313	2 S59448	hypothetical prote
2	18	69.2	480	2 E75433	hypothetical prote
3	17	65.4	194	2 JQ1560	hypothetical 20.6K
4	17	65.4	220	2 JC4082	coat protein - Cym
5	17	65.4	376	2 AB2920	cobalamin biosynth
6	17	65.4	388	2 C97694	cobalamin biosynth
7	17	65.4	389	2 T23167	hypothetical prote
8	17	65.4	570	2 T37314	probable kexin (EC
9	17	65.4	634	2 S33575	dnaK-type molecula
10	17	65.4	942	2 DB7803	protein bli-4D [im
11	17	65.4	2704	2 S09118	G surface protein
12	16	61.5	71	2 F84312	hypothetical prote
13	16	61.5	85	2 E70531	hypothetical prote
14	16	61.5	104	2 S51479	drought-induced pr
15	16	61.5	105	2 A71249	hypothetical prote
16	16	61.5	108	2 F72549	hypothetical prote
17	16	61.5	126	2 A23473	chymotrypsin-like
18	16	61.5	129	2 T49498	hypothetical prote
19	16	61.5	133	2 A96746	hypothetical prote
20	16	61.5	147	2 S09762	hypothetical prote
21	16	61.5	153	2 PN0103	hypothetical 17K p
22	16	61.5	161	2 T28088	hypothetical prote
23	16	61.5	164	2 JQ1252	hypothetical 16.7K
24	16	61.5	229	2 T34277	hypothetical prote
25	16	61.5	242	2 A45724	pectate lyase (EC
26	16	61.5	244	2 S72219	chymotrypsin B - A
27	16	61.5	251	2 A55035	cysteine-rich prot
28	16	61.5	262	1 JQ1724	E1 membrane glycop
29	16	61.5	263	2 S47537	chymotrypsin (EC 3

30 16 61.5 275 2 G91011 probable elongatio  
31 16 61.5 275 2 A85856 probable elongatio  
32 16 61.5 275 2 B64986 hypothetical 30.9  
33 16 61.5 294 2 T23682 hypothetical prote  
34 16 61.5 306 2 C71498 probable yop trans  
35 16 61.5 317 2 T00500 probable elicitor  
36 16 61.5 321 2 A84792 hypothetical prote  
37 16 61.5 349 2 JE0202 paired-box-contain  
38 16 61.5 380 2 T04007 hypothetical prote  
39 16 61.5 397 2 T26077 hypothetical prote  
40 16 61.5 422 2 S41514 RAD52 protein homo  
41 16 61.5 473 2 C81039 lipopolysaccharide  
42 16 61.5 473 2 C81984 probable lipopolys  
43 16 61.5 475 2 T36342 probable glutamate  
44 16 61.5 486 2 B86460 hypothetical prote  
45 16 61.5 510 2 A55207 glycerol-3-phospha

ALIGNMENTS

RESULT 1  
S59448  
hypothetical protein YMR206w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YM8325.07  
C;Species: Saccharomyces cerevisiae  
C;Date: 30-Nov-1995 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: S59448  
R;Odell, C.; Bowman, S.  
submitted to the EMBL Data Library, March 1995  
A;Reference number: S59441  
A;Accession: S59448  
A;Molecule type: DNA  
A;Residues: 1-313 <ODE>  
A;Cross-references: UNIPROT:Q03695; EMBL:Z48755; NID:g7336296; PIDN:CAA88648.1; PID:g733630  
A;Experimental source: strain AB972  
C;Genetics:  
A;Gene: MIPS:YMR206w  
A;Cross-references: SGD:S0004819  
A;Map position: 13R

Query Match 69.2%; Score 18; DB 2; Length 313;  
Best Local Similarity 20.0%; Pred. No. 0.49;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
|  
Db 245 CSSSSSSSSAC 254

RESULT 2  
E75433  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: E75433  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; H  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: E75433  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-480 <WHI>  
A;Cross-references: UNIPROT:Q9RV87; GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AAF10716  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR1142  
A;Map position: 1  
C;Superfamily: Deinococcus radiodurans hypothetical protein DR1142

Query Match		69.2%;	Score 18;	DB 2;	Length 480;
Best Local Similarity		20.0%;	Pred. No. 0.56;		
Matches	2;	Conservative	0;	Mismatches	8; Indels 0; Gaps 0;
QY	1	CXXXXXXXXC 10			
Db	464	CASAAATAAC 473			
RESULT 3					
JQ1560					
hypotheical 20.6K protein - Lymantria dispar nuclear polyhedrosis virus					
N;Alternate names: hypothetical protein 4					
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV					
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004					
C;Accession: JQ1560					
R;Bjornson, R.M.; Rohrmann, G.F.					
J. Gen. Virol. 73, 1499-1504, 1992					
A;Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymantria					
A;Reference number: PQ0339; MUID:92300345; PMID:1607868					
A;Accession: JQ1560					
A;Molecule type: DNA					
A;Residues: 1-194 <BJO>					
A;Cross-references: UNIPROT:P36868; DDBJ:D10836					
Query Match		65.4%;	Score 17;	DB 2;	Length 194;
Best Local Similarity		20.0%;	Pred. No. 1.7;		
Matches	2;	Conservative	0;	Mismatches	8; Indels 0; Gaps 0;
QY	1	CXXXXXXXXC 10			
Db	74	CSAAMTSSSC 83			
RESULT 4					
JC4082					
coat protein - Cymbidium mosaic virus					
C;Species: Cymbidium mosaic virus					
C;Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004					
C;Accession: JC4082					
R;Ryu, K.H.; Yoon, K.E.; Park, W.M.					
Gene 156, 303-304, 1995					
A;Title: Cloning and sequencing of a cDNA encoding the coat protein of a Korean isolate					
A;Reference number: JC4082; MUID:95278762; PMID:7758973					
A;Accession: JC4082					
A;Molecule type: mRNA					
A;Residues: 1-220 <RYU>					
A;Cross-references: UNIPROT:Q66152; EMBL:X81051; NID:g897718; PIDN:CAAS6941.1; PID:g897718					
A;Note: The authors translated the codon GTG for residue 161 as Leu					
C;Superfamily: potato virus coat protein					
C;Keywords: coat protein					
Query Match		65.4%;	Score 17;	DB 2;	Length 220;
Best Local Similarity		20.0%;	Pred. No. 1.8;		
Matches	2;	Conservative	0;	Mismatches	8; Indels 0; Gaps 0;
QY	1	CXXXXXXXXC 10			
Db	166	CSAATLTATC 175			
RESULT 5					
AB2920					
cobalamin biosynthetic protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont					
C;Species: Agrobacterium tumefaciens					
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004					
C;Accession: AB2920					
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Gillet, W.; Grant, C.; Guenther, D.; Kutya, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.					
Science 294, 2317-2323, 2001					
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.					

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.								
A;Reference number: AB2577; MUID:21608550; PMID:11743193								
A;Accession: AB2920								
A;Status: preliminary								
A;Molecule type: DNA								
A;Residues: 1-376 <KUR>								
A;Cross-references: UNIPROT:Q8UBQ6; GB:AE008688; PIDN:AAL43776.1; PID:g17741313; GSPDB:GN00020								
A;Experimental source: strain C58 (Dupont)								
C;Genetics:								
A;Gene: cbiD								
A;Map position: circular chromosome								
C;Superfamily: Methanobacterium cobalamin biosynthesis protein D								
Query Match		65.4%;	Score 17;	DB 2;	Length 376;			
Best Local Similarity		20.0%;	Pred. No. 2.2;					
Matches	2;	Conservative	0;	Mismatches	8; Indels 0; Gaps 0;			
QY	1	CXXXXXXXXC 10						
Db	17	CAAAATKAAC 26						
RESULT 6								
C97694								
cobalamin biosynthetic protein cbiD (PA2908) [imported] - Agrobacterium tumefaciens (strain C58)								
C;Species: Agrobacterium tumefaciens								
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004								
C;Accession: C97694								
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001								
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens								
A;Reference number: A97359; MUID:21608551; PMID:11743194								
A;Accession: C97694								
A;Status: preliminary								
A;Molecule type: DNA								
A;Residues: 1-388 <KUR>								
A;Cross-references: UNIPROT:Q8UBQ6; GB:AE007869; PIDN:AAK88508.1; PID:g15158019; GSPDB:GN00020								
C;Genetics:								
A;Gene: AGR_C_5073								
A;Map position: circular chromosome								
C;Superfamily: Methanobacterium cobalamin biosynthesis protein D								
Query Match		65.4%;	Score 17;	DB 2;	Length 388;			
Best Local Similarity		20.0%;	Pred. No. 2.2;					
Matches	2;	Conservative	0;	Mismatches	8; Indels 0; Gaps 0;			
QY	1	CXXXXXXXXC 10						
Db	29	CAAAATKAAC 38						
RESULT 7								
T23167								
hypothetical protein K01C8.2 - Caenorhabditis elegans								
C;Species: Caenorhabditis elegans								
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004								
C;Accession: T23167								
R;Sims, M.								
submitted to the EMBL Data Library, April 1995								
A;Reference number: Z19702								
A;Accession: T23167								
A;Status: preliminary; translated from GB/EMBL/DDBJ								
A;Molecule type: DNA								
A;Residues: 1-389 <WIL>								
A;Cross-references: UNIPROT:Q21081; EMBL:Z49068; PIDN:CAA8855.1; GSPDB:GN00020; CESP:K01C8								
A;Experimental source: clone K01C8								
C;Genetics:								
A;Gene: CESP:K01C8.2								
A;Map position: 2								
A;Introns: 54/2; 146/3; 208/3; 283/1; 379/3								
Query Match		65.4%;	Score 17;	DB 2;	Length 389;			

Best Local Similarity 20.0%; Pred. No. 2.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 123 CSSSISTSSC 132

RESULT 8  
T37314  
probable kexin (EC 3.4.21.61) - Caenorhabditis elegans (fragment)  
N;Alternate names: blisterase 4  
C;Species: Caenorhabditis elegans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C;Accession: T37314  
R;Thacker, C.; Peters, K.; Srayko, M.; Rose, A.M.  
Genes Dev. 9, 956-971, 1995  
A;Title: The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/su  
A;Reference number: Z21679; MUID:95293228; PMID:7774813  
A;Accession: T37314  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-570 <THA>  
A;Cross-references: EMBL:L29440; NID:g459702; PIDN:AAA98752.1; PID:g459703  
C;Genetics:  
A;Gene: bli-4  
A;Map position: I  
C;Keywords: alternative splicing; hydrolase; serine proteinase

Query Match 65.4%; Score 17; DB 2; Length 570;  
Best Local Similarity 20.0%; Pred. No. 2.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 311 CTESSSATSC 320

RESULT 9  
S33575  
dnaK-type molecular chaperone precursor, mitochondrial - Leishmania major  
N;Alternate names: heat shock protein 70-related protein; mitochondrial stress protein  
C;Species: Leishmania major  
C;Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: S33575; S78090; S05438  
R;Searle, S.; McCrossan, M.V.; Smith, D.F.  
J. Cell Sci. 104, 1091-1100, 1993  
A;Title: Expression of a mitochondrial stress protein in the protozoan parasite Leishman  
A;Reference number: S33575; MUID:93300981; PMID:8314893  
A;Accession: S33575  
A;Molecule type: DNA  
A;Residues: 1-634 <SEA>  
A;Cross-references: UNIPROT:P12076; EMBL:X64137  
R;Smith, D.F.  
submitted to the EMBL Data Library, January 1992  
A;Reference number: S78090  
A;Accession: S78090  
A;Molecule type: DNA  
A;Residues: 1-460,481-500,'QGERETIASENQIRGEFDLSG',501-634 <SMI>  
A;Cross-references: EMBL:X64137; NID:g311289; PIDN:CAA45498.1; PID:g311290  
R;Searle, S.; Campos, A.J.R.; Coulson, R.M.R.; Spithill, T.W.; Smith, D.F.  
Nucleic Acids Res. 17, 5081-5095, 1989  
A;Title: A family of heat shock protein 70-related genes are expressed in the promastig  
A;Reference number: S05438; MUID:89345072; PMID:2762121  
A;Accession: S05438  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-249 <SEF>  
A;Cross-references: EMBL:X14574; NID:g9561; PIDN:CAA32713.1; PID:g9562  
C;Genetics:  
A;Gene: Lmhsp70.1  
A;Genome: nuclear  
C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein comple  
C;Superfamily: heat shock protein 70  
C;Keywords: ATP; mitochondrion; molecular chaperone; stress-induced protein  
F;1-23/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
F;24-634/Product: heat shock protein 70, mitochondrial #status predicted <MAT>

Query Match 65.4%; Score 17; DB 2; Length 634;  
Best Local Similarity 20.0%; Pred. No. 2.6;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 7 CGSAAASAAC 16

RESULT 10  
D87803  
protein bli-4D [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 21-Jun-2002  
C;Accession: D87803  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: D87803  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-942 <STO>  
A;Cross-references: GB:chr\_I; PIDN:AAB96754.1; PID:g2773243; GSPDB:GN00019  
C;Genetics:  
A;Gene: bli-4D  
A;Map position: 1  
C;Superfamily: kexin; subtilisin homology

Query Match 65.4%; Score 17; DB 2; Length 942;  
Best Local Similarity 20.0%; Pred. No. 3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 683 CTESSSATSC 692

RESULT 11  
S09118  
G surface protein 168 - Paramecium primaurelia  
C;Species: Paramecium primaurelia  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: S09118  
R;Prat, A.  
J. Mol. Biol. 211, 521-535, 1990  
A;Title: Conserved sequences flank variable tandem repeats in two alleles of the G surfac  
A;Reference number: S09118; MUID:90172419; PMID:2308165  
A;Accession: S09118  
A;Molecule type: DNA  
A;Residues: 1-2704 <PRA>  
A;Cross-references: UNIPROT:P17053; EMBL:X52133; NID:g10049; PIDN:CAA36378.1; PID:g57847;  
C;Genetics:  
A;Genetic code: SGC5  
C;Superfamily: G surface protein

Query Match 65.4%; Score 17; DB 2; Length 2704;  
Best Local Similarity 20.0%; Pred. No. 4.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10  
Db 1632 CVAATAATTC 1641

RESULT 12  
F84312  
hypothetical protein Vng1598h [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: F84312  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.  
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: F84312  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-71 <STO>  
A;Cross-references: UNIPROT:Q9HPK1; GB:AE004437; NID:g10581076; PIDN:AAG19866.1; GSPDB:G  
C;Genetics:  
A;Gene: VNG1598H

Query Match 61.5%; Score 16; DB 2; Length 71;  
Best Local Similarity 20.0%; Pred. No. 5.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 30 CSRSVSTSTC 39

RESULT 13  
E70531  
hypothetical protein Rv2706c - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: E70531  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: E70531  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-85 <COL>  
A;Cross-references: UNIPROT:O07207; GB:Z96072; GB:AL123456; NID:g3261793; PIDN:CAB09466.  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv2706c

Query Match 61.5%; Score 16; DB 2; Length 85;  
Best Local Similarity 20.0%; Pred. No. 5.4;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 24 CSATAVAAVC 33

RESULT 14  
S51479  
drought-induced protein Di21 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 15-Jul-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S51479; S43176  
R;Gosti, F.; Bertauche, N.; Vartanian, N.; Giraudat, J.  
Mol. Gen. Genet. 246, 10-18, 1995  
A;Title: Abscissic acid-dependent and -independent regulation of gene expression by progr  
A;Reference number: S51478; MUID:95124290; PMID:7823904  
A;Accession: S51479  
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA  
A;Residues: 1-104 <GOS>  
A;Cross-references: UNIPROT:Q39084; EMBL:X78585; NID:g469111; PIDN:CAA55322.1; PID:g46911  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994  
C;Genetics:  
A;Gene: Di21  
C;Superfamily: late embryogenesis-abundant protein leas

Query Match 61.5%; Score 16; DB 2; Length 104;  
Best Local Similarity 20.0%; Pred. No. 5.8;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 14 CSAASGSLSC 23

RESULT 15  
A71249  
hypothetical protein PH0248 - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C;Accession: A71249  
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: A71249  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-105 <KAW>  
A;Cross-references: UNIPROT:O57986; GB:AP0000001; NID:g3236128; PIDN:BAA29320.1; PID:g325  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH0248

Query Match 61.5%; Score 16; DB 2; Length 105;  
Best Local Similarity 20.0%; Pred. No. 5.8;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 35 CFTASASLAC 44

Search completed: December 30, 2004, 13:17:10  
Job time : 14.6761 secs



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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	213	2 Q96KM3	Q96km3 homo sapien
2	18	69.2	283	2 Q7PRQ7	Q7prq7 anopheles g
3	18	69.2	313	1 YM58 YEAST	Q03695 saccharomyc
4	18	69.2	357	2 Q6ZDR4	Q6zdr4 oryza sativ
5	18	69.2	357	2 BAD09322	Bad09322 oryza sat
6	18	69.2	480	2 Q9RV87	Q9rv87 deinococcus
7	18	69.2	653	2 Q8IXM8	Q8ixm8 homo sapien
8	17	65.4	52	2 Q8LPD6	Q8lpd6 hordeum vul
9	17	65.4	128	2 Q96LJ4	Q96lj4 homo sapien
10	17	65.4	139	2 Q6ZKM7	Q6zkm7 oryza sativ
11	17	65.4	139	2 BAD08805	Bad08805 oryza sat
12	17	65.4	155	2 Q6H482	Q6h482 oryza sativ
13	17	65.4	219	2 Q825E8	Q825e8 streptomyce
14	17	65.4	220	2 Q661S2	Q661s2 cymbidium m
15	17	65.4	256	2 Q6YTS2	Q6yts2 oryza sativ
16	17	65.4	256	2 BAD10719	Bad10719 oryza sat
17	17	65.4	260	2 Q850Z3	Q850z3 oryza sativ
18	17	65.4	368	2 Q7ORD3	Q7ord3 gerbera hyb
19	17	65.4	368	2 CAD87007	Cad87007 gerbera h
20	17	65.4	376	1 CEID AGRT5	Q8ubq6 agrobacteri
21	17	65.4	388	2 Q7PYI3	Q7pyi3 anopheles g
22	17	65.4	389	2 Q21081	Q21081 caenorhabdi
23	17	65.4	471	2 Q9VMG7	Q9vmg7 drosophila
24	17	65.4	475	2 Q7X7A4	Q7x7a4 oryza sativ
25	17	65.4	475	2 CAE04361	Cae04361 oryza sat
26	17	65.4	475	2 CAE04825	Cae04825 oryza sat
27	17	65.4	556	2 Q803D5	Q803d5 brachydanio
28	17	65.4	634	1 HS71 LEIMA	P12076 leishmania
29	17	65.4	699	2 Q8I9F8	Q8i9p8 corbicula f
30	17	65.4	699	2 AA017927	Aa017927 corbicula
31	17	65.4	734	2 Q9NKE3	Q9nke3 drosophila

32	17	65.4	843	2 Q80GV2	Q80gv2 hepatitis b
33	17	65.4	943	1 BLI4 CAEEL	PS1559 caenorhabdi
34	17	65.4	1056	2 Q7QE80	Q7qe80 anopheles g
35	17	65.4	1130	2 Q9H1V5	Q9h1v5 homo sapien
36	17	65.4	1347	2 Q6CCI6	Q6ccic yarrowia li
37	17	65.4	2704	1 G168 PARPR	P17053 paramecium
38	17	65.4	2717	2 Q947I0	Q947i0 paramecium
39	17	65.4	2721	2 Q76973	Q76973 paramecium
40	17	65.4	2729	2 Q6PQK6	Q6pgk6 paramecium
41	17	65.4	2729	2 AAS94225	Aas94225 parameciu
42	16	61.5	68	2 Q6JL92	Q6jl92 neisseria g
43	16	61.5	68	2 AAS16526	Aas16526 neisseria
44	16	61.5	71	2 Q9HPK1	Q9hpk1 halobacteri
45	16	61.5	80	2 Q6IGD0	Q6igd0 drosophila

ALIGNMENTS

RESULT 1  
Q96KM3  
ID Q96KM3 PRELIMINARY; PRT; 213 AA.  
AC Q96KM3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Aberrant WM domain-containing oxidoreductase.  
GN Name=WVOX;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21457335; PubMed=11572989;  
RA Paige A.J.W., Taylor K.J., Taylor C., Hallier S.G., Farrington S.,  
RA Scott D., Porteous D.J., Smyth J.F., Gabra H., Watson J.E.V.;  
RT "WVOX: a candidate tumor suppressor gene involved in multiple tumor  
types.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:11417-11422(2001).  
DR EMBL; AF325432; AAL05451.1; -.  
DR EMBL; AF325423; AAL05451.1; JOINED.  
DR EMBL; AF325424; AAL05451.1; JOINED.  
DR EMBL; AF325426; AAL05451.1; JOINED.  
DR EMBL; AF325433; AAL05451.1; JOINED.  
DR EMBL; AF325425; AAL05451.1; JOINED.  
DR HSSP; Q13526; IPIN.  
DR InterPro; IPR001202; WW\_Rep5\_WWP.  
DR Pfam; PF00397; WW; 2.  
DR SMART; SM00456; WW; 2.  
DR PROSITE; PS01159; WW\_DOMAIN\_1; 2.  
DR PROSITE; PS50020; WW\_DOMAIN\_2; 2.  
SQ SEQUENCE 213 AA; 23868 MW; A21054FF8214CC7C CRC64;

Query Match 69.2%; Score 18; DB 2; Length 213;  
Best Local Similarity 20.0%; Pred. No. 0.66;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
Db 184 CTSTTAAAC 193

RESULT 2  
Q7PRQ7  
ID Q7PRQ7 PRELIMINARY; PRT; 283 AA.  
AC Q7PRQ7;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ENSANGP0000001657 (Fragment).  
GN Name=ENSANGG0000001387;  
OS Anopheles gambiae str. PEST.

```
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008847; EAA06779.2; -.
DR InterPro; IPR000877; Prot_inh_BBI.
DR PROSITE; PS00281; BOWMAN_BIRK; UNKNOWN_2.
FT NON_TER 1
FT NON_TER 283
SQ SEQUENCE 283 AA; 25479 MW; EF5695EI9584D5F2 CRC64;

Query Match          69.2%; Score 18; DB 2; Length 283;
Best Local Similarity 20.0%; Pred. No. 0.74;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 163 CASSSSTTSC 172

RESULT 3
YM58 YEAST          STANDARD; PRT; 313 AA.
ID _YM58 YEAST          STANDARD; PRT; 313 AA.
AC Q03695;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 35.0 kDa protein in PFK2-HPA1 intergenic region.
GN OrderedLocusNames=YMR206W; ORFNames=YMG325.07;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).
CC -!- SIMILARITY: SOME, TO YEAST YNR014W.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z48755; CAA88648.1; -.
DR PIR; S59448; S59448.
DR GernOnline; 142881; -.
DR SGD; S0004819; YMR206W.
KW Hypothetical protein.
FT DOMAIN 3 6 Poly-Ser.
FT DOMAIN 146 149 Poly-Gln.
FT DOMAIN 246 252 Poly-Ser.
SQ SEQUENCE 313 AA; 35017 MW; 9D92BFDE982577F0 CRC64;

Query Match          69.2%; Score 18; DB 1; Length 313;
Best Local Similarity 20.0%; Pred. No. 0.77;

us-10-046-922-33.rup
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Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 245 CSSSSSSSSAC 254

RESULT 4
Q6ZDR4
ID Q6ZDR4          PRELIMINARY; PRT; 357 AA.
AC Q6ZDR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transcription factor Myb protein.
GN Name=P0481F05.20;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 2 Myb-like domains.
DR EMBL; AP004376; BAD09322.1; -.
DR InterPro; IPR009057; Homeodomain like.
DR InterPro; IPR001005; Myb DNA binding.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
KW Nuclear protein.
SQ SEQUENCE 357 AA; 36754 MW; 3F4F56860D3B4E22 CRC64;

Query Match          69.2%; Score 18; DB 2; Length 357;
Best Local Similarity 20.0%; Pred. No. 0.81;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 322 CSATASASSC 331

RESULT 5
BAD09322
ID BAD09322          PRELIMINARY; PRT; 357 AA.
AC BAD09322;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transcription factor Myb protein.
GN P0481F05.20.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza; Oryza sativa.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC
RT clone:P0481F05.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004376; BAD09322.1; -.
SQ SEQUENCE 357 AA; 36754 MW; 3F4F56860D3B4E22 CRC64;

Query Match          69.2%; Score 18; DB 2; Length 357;
Best Local Similarity 20.0%; Pred. No. 0.81;
```

Matches	2;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;
Qy	1	CXXXXXXXXC 10							
Db	322	CSATASASC 331							
RESULT 6									
Q9RV87									
ID	Q9RV87	PRELIMINARY;	PRT;	480	AA.				
AC	Q9RV87;								
DT	01-MAY-2000	(TrEMBLrel. 13, Created)							
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)							
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)							
DE	Hypothetical protein DR1142.								
GN	OrderedLocusNames=DR1142;								
OS	Deinococcus radiodurans.								
OC	Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;								
OC	Deinococcaceae; Deinococcus.								
OX	NCBI_TaxID=1299;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;								
RX	MEDLINE=20036896; PubMed=10567266;								
RA	White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,								
RA	Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,								
RA	Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,								
RA	Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,								
RA	Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,								
RA	Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,								
RA	Fraser C.M.;								
RT	"Genome sequence of the radioresistant bacterium Deinococcus								
RT	radiodurans R1.";								
RL	Science 286:1571-1577(1999).								
DR	EMBL; AE001963; AAF10716.1; -.								
DR	PIR; E75433; E75433.								
DR	TIGR; DR1142; -.								
KW	Complete proteome; Hypothetical protein.								
SQ	SEQUENCE 480 AA; 49364 MW; 18B962ADA5CA24AE CRC64;								
Query Match 69.2%; Score 18; DB 2; Length 480;									
Best Local Similarity 20.0%; Pred. No. 0.91;									
Matches	2;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;
Qy	1	CXXXXXXXXC 10							
Db	464	CASAAATAAC 473							
RESULT 7									
Q8IXM8									
ID	Q8IXM8	PRELIMINARY;	PRT;	653	AA.				
AC	Q8IXM8;								
DT	01-MAR-2003	(TrEMBLrel. 23, Created)							
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)							
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)							
DE	KIAA0779 protein.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Skin;								
RX	MEDLINE=22388257; PubMed=12477932;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,								
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,								
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,								

RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,									
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,									
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,									
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,									
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,									
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,									
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,									
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,									
RA	Jones S.J., Marra M.A.;									
RT	"Generation and initial analysis of more than 15,000 full-length human									
RT	and mouse cDNA sequences.";									
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).									
RN	[2]									
RP	SEQUENCE FROM N.A.									
RC	TISSUE=Skin;									
RA	Strausberg R.;									
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.									
DR	EMBL; BC039859; AAH39859.1; -.									
SQ	SEQUENCE 653 AA; 72052 MW; 18B07D171E874205 CRC64;									
Query Match 69.2%; Score 18; DB 2; Length 653;										
Best Local Similarity 20.0%; Pred. No. 1;										
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;										
Qy	1 CXXXXXXXXC 10									
Db	173 CAAAAAAAC 182									
RESULT 8										
Q8LPD6										
ID	Q8LPD6	PRELIMINARY;		PRT; 52 AA.						
AC	Q8LPD6;									
DT	01-OCT-2002 (TrEMBLrel. 22, Created)									
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)									
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)									
DE	Putative glutathione-S-transferase (Fragment).									
GN	Name=bar2;									
OS	Hordeum vulgare (Barley).									
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;									
OC	Triticeae; Hordeum.									
OX	NCBI_TaxID=4513;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RA	Baldwin A.;									
RT	"The effect of thiocarbamate herbicides and the safener dichlormid in									
RT	barley and wild oats.";									
RL	Thesis (2001), Department of Cardiff School of Biosciences, Cardiff									
RL	university, Cardiff, United Kingdom.									
RN	[2]									
RP	SEQUENCE FROM N.A.									
RA	Baldwin A., Harwood J.L., Machray G.C., Francis D., Rogers H.J.;									
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.									
DR	EMBL; AJ419772; CAD11963.1; -.									
DR	HSSP; P12653; 1AXD.									
DR	GO; GO:0003700; F:transcription factor activity; IEA.									
DR	GO; GO:0016740; F:transferase activity; IEA.									
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.									
DR	InterPro; IPR002197; HTH_Fis.									
DR	PRINTS; PR01590; HTHFIS.									
KW	Transferase.									
FT	NON_TER	1								
FT	NON_TER	52								
SQ	SEQUENCE	52 AA;	5750 MW;	7392EB72A3C70B9B	CRC64;					
Query Match 65.4%; Score 17; DB 2; Length 52;										
Best Local Similarity 20.0%; Pred. No. 1.9;										
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;										
Qy	1 CXXXXXXXXC 10									
Db	18 CTSASSTRSC 27									

RESULT 9  
Q96LJ4  
ID Q96LJ4 PRELIMINARY; PRT; 128 AA.  
AC Q96LJ4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein FLJ25437.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,  
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,  
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,  
RA Sugano S.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK058166; BAB71697.1; --  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004672; F:protein kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding.  
SQ SEQUENCE 128 AA; 14115 MW; D30AC8C668621B0C CRC64;

Query Match 65.4%; Score 17; DB 2; Length 128;  
Best Local Similarity 20.0%; Pred. No. 2.6;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 118 CTATSSAKTC 127

RESULT 10  
Q6ZKM7  
ID Q6ZKM7 PRELIMINARY; PRT; 139 AA.  
AC Q6ZKM7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein OJ1118\_A06.7-1.  
GN Name=OJ1118\_A06.7-1;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP003873; BAD08805.1; --  
KW Hypothetical protein.  
SQ SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;

Query Match 65.4%; Score 17; DB 2; Length 139;  
Best Local Similarity 20.0%; Pred. No. 2.7;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|

Db 77 CAAITSSSSC 86  
RESULT 11  
BAD08805  
ID BAD08805 PRELIMINARY; PRT; 139 AA.  
AC BAD08805;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein OJ1118\_A06.7-1.  
GN OJ1118\_A06.7-1.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza; Oryza sativa.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC  
clone:OJ1118\_A06.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP003873; BAD08805.1; --  
KW Hypothetical protein.  
SQ SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;

Query Match 65.4%; Score 17; DB 2; Length 139;  
Best Local Similarity 20.0%; Pred. No. 2.7;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 77 CAAITSSSSC 86

RESULT 12  
Q6H482  
ID Q6H482 PRELIMINARY; PRT; 155 AA.  
AC Q6H482;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein OJ1119\_C03.6.  
GN Name=OJ1119\_C03.6;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Hattori M., Sasaki Y., Katayose Y.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP005969; BAD26467.1; --  
KW Hypothetical protein.  
SQ SEQUENCE 155 AA; 16233 MW; 02D836E5E8C77B52 CRC64;

Query Match 65.4%; Score 17; DB 2; Length 155;  
Best Local Similarity 20.0%; Pred. No. 2.8;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 25 CSTTSAADC 34

RESULT 13  
Q825E8  
ID Q825E8 PRELIMINARY; PRT; 219 AA.  
AC Q825E8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)



DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Putative TetR-family transcriptional regulator.  
GN OrderedLocusNames=SAV7510;  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
RT avermitilis: deducing the ability of producing secondary  
RT metabolites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680;  
RX MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
RA Sakaki Y., Hattori M., Omura S.;  
RT "Complete genome sequence and comparative analysis of the industrial  
RT microorganism Streptomyces avermitilis.";  
RL Nat. Biotechnol. 21:526-531(2003).  
DR EMBL; AP005050; BAC75221.1; -.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR InterPro; IPR001647; HTH\_Tetr.  
DR Pfam; PF00440; Tetr\_N; 1.  
KW Complete proteome.  
SQ SEQUENCE 219 AA; 24066 MW; 5C59ADF39430F304 CRC64;  
  
Query Match 65.4%; Score 17; DB 2; Length 219;  
Best Local Similarity 20.0%; Pred. No. 3.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXXC 10  
Db 151 CAEAAAAAAC 160  
  
RESULT 14  
Q66152 ID Q66152 PRELIMINARY; PRT; 220 AA.  
AC Q66152;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Coat protein.  
OS Cymbidium mosaic virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;  
OC Potexvirus.  
OX NCBI\_TaxID=12178;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Korean isolate;  
RX MEDLINE=95278762; PubMed=7758973;  
RA Ryu K.H., Yoon K.E., Park W.M.;  
RT "Nucleotide sequence of coat protein gene of cymbidium mosaic  
RT potexvirus genomic RNA, the Korean isolate.";  
RL Gene 156:303-304(1995).  
CC -1- SIMILARITY: Belongs to the potexviruses coat protein family.  
DR EMBL; X81051; CAA56941.1; -.  
DR PIR; JC4082; JC4082.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000052; PltVir\_coat.  
DR Pfam; PF00286; Virus\_P-coat; 1.

DR PRINTS; PR00232; POTXCARLCOAT.  
DR ProDom; PD000603; PltVir\_coat; 1.  
KW Coat protein.  
SQ SEQUENCE 220 AA; 23719 MW; 1F40C6E7CDCCF3B8 CRC64;  
  
Query Match 65.4%; Score 17; DB 2; Length 220;  
Best Local Similarity 20.0%; Pred. No. 3.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXXC 10  
Db 166 CSAATLTATC 175  
  
RESULT 15  
Q6YTS2 ID Q6YTS2 PRELIMINARY; PRT; 256 AA.  
AC Q6YTS2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein P0419H09.29.  
GN Name=P0419H09.29;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP005918; BAD10719.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 256 AA; 26591 MW; 63BFCAF53D2D40EA CRC64;  
  
Query Match 65.4%; Score 17; DB 2; Length 256;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXXC 10  
Db 203 CSASASAARC 212  
  
Search completed: December 30, 2004, 13:16:04  
Job time : 95.2641 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:19:46 ; Search time 94 Seconds  
(without alignments)  
38.163 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	96.4	10	5	ABP53931
2	54	96.4	10	5	ABP53932
3	33	58.9	7	5	ABP53964
4	33	58.9	8	5	ABP53965
5	33	58.9	10	5	ABP53968
6	32	57.1	7	3	AAV76794
7	32	57.1	7	5	ABP53418
8	31	55.4	8	2	AAW97529
9	31	55.4	9	5	ABP53933
10	31	55.4	9	8	ADN64476
11	31	55.4	10	4	AAG95260
12	30.5	54.5	10	2	AAV14709
13	30	53.6	9	4	AAU02369
14	30	53.6	9	4	AAU02282
15	30	53.6	10	4	AAV99759
16	30	53.6	10	8	ADG94728
17	30	53.6	10	8	ADI47102
18	30	53.6	10	8	ADP87303
19	29	51.8	5	2	AAV29452
20	29	51.8	5	2	AAV69224
21	29	51.8	5	2	AAW56531
22	29	51.8	7	8	ADJ25834
23	29	51.8	8	4	ABP22594
24	29	51.8	8	4	ABP14287
25	29	51.8	8	4	ABP18686

26	29	51.8	8	4	ABP20292	Abp20292 HIV A03 m
27	29	51.8	8	4	ABP19992	Abp19992 HIV A03 m
28	29	51.8	8	4	ABP12050	Abp12050 HIV A02 s
29	29	51.8	8	4	ABP14288	Abp14288 HIV A03 s
30	29	51.8	8	4	ABP16999	Abp16999 HIV B27 s
31	29	51.8	8	4	ABP22402	Abp22402 HIV A11 m
32	29	51.8	8	7	ADL17320	ADL17320 DENGIN-18
33	29	51.8	8	8	ADH62133	Adh62133 Cyclic an
34	29	51.8	8	8	ADH62029	Adh62029 Cyclic an
35	29	51.8	8	8	ADH62062	Adh62062 Cyclic an
36	29	51.8	8	8	ADP67844	Adp67844 Anti-micr
37	29	51.8	8	8	ADP67877	Adp67877 Anti-micr
38	29	51.8	8	8	ADP67948	Adp67948 Anti-micr
39	29	51.8	8	8	ADQ28160	Adq28160 Excluded
40	29	51.8	8	8	ADQ28097	Adq28097 Excluded
41	29	51.8	8	8	ADQ28067	Adq28067 Excluded
42	29	51.8	9	2	AAV37115	Aar37115 HIV envel
43	29	51.8	9	2	AAV37113	Aar37113 HIV envel
44	29	51.8	9	2	AAV73059	Aar73059 Antigen f
45	29	51.8	9	2	AAV43338	Aaw43338 Immunogen

ALIGNMENTS

RESULT 1  
ABP53931  
ID ABP53931 standard; peptide; 10 AA.  
XX  
AC ABP53931;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:34.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytotstatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX Homo sapiens.  
OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "any amino acid"  
FT Misc-difference 10 /note= "any amino acid"  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB0000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX WPI; 2002-691521/74.  
DR  
XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 12; Page 80; 149pp; English.  
XX The present invention describes an isolated peptide (I) that binds to and  
CC

CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 96.4%; Score 54; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.091;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
Db 2 GYWLTIWG 9  
| | | | | | | |  
  
RESULT 2  
ABP53932  
ID ABP53932 standard; peptide; 10 AA.  
XX  
AC ABP53932;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:35.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnerary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 13; Page 80; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 96.4%; Score 54; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.091;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
Db 2 GYWLTIWG 9  
| | | | | | | |  
  
RESULT 3  
ABP53964  
ID ABP53964 standard; peptide; 7 AA.  
XX  
AC ABP53964;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:67.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnerary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 4..6  
FT /note= "X is any amino acid"  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 21; Page 81; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,

CC	skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC	neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC	chronic hepatitis, haemangiomas and diabetes. The present sequence
CC	represents a specifically claimed VEGFR-3 binding peptide from the
CC	present invention
XX	
SQ	Sequence 7 AA;
Query Match 58.9%; Score 33; DB 5; Length 7;	
Best Local Similarity 57.1%; Pred. NO. 1.7e+06;	
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 GYWLTIW 8
Db	1 GYWXXXW 7
RESULT 4	
ABP53965	
ID	ABP53965 standard; peptide; 8 AA.
XX	
AC	ABP53965;
XX	
DT	09-JAN-2003 (first entry)
XX	
DE	VEGFR-3 binding peptide SEQ ID NO:68.
XX	
KW	Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW	angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW	cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW	vulnary; cell surface receptor; cancer; neovascularisation;
KW	liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW	diabetes; PDGF; platelet derived growth factor.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 4. .6 /note= "X is any amino acid"
FT	
FT	Misc-difference 8 /note= "any amino acid"
FT	
XX	
PN	WO200257299-A2.
XX	
PD	25-JUL-2002.
XX	
PF	16-JAN-2002; 2002WO-IB000099.
XX	
PR	17-JAN-2001; 2001US-0262476P.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(LICN ) LICENTIA LTD.
XX	
PI	Alitalo K, Koivunen E, Kubo H;
XX	
DR	WPI; 2002-691521/74.
XX	
PT	New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT	diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT	such as cancer and diseases of neovascularization.
XX	
PS	Claim 22; Page 81; 149pp; English.
XX	
CC	The present invention describes an isolated peptide (I) that binds to and
CC	inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC	have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC	antidiabetic and vulnary activities, and can be used in gene therapy.
CC	Compositions and methods from the present invention are useful for
CC	diagnosing, evaluating and treating disorders mediated by the activity of
CC	the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC	liver, spleen, kidney, lymph node, small intestine, blood cells,
CC	pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,

---

CC	skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC	neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC	chronic hepatitis, haemangiomas and diabetes. The present sequence
CC	represents a specifically claimed VEGFR-3 binding peptide from the
CC	present invention
XX	
SQ	Sequence 8 AA;
Query Match 58.9%; Score 33; DB 5; Length 8;	
Best Local Similarity 57.1%; Pred. NO. 1.7e+06;	
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 GYWLTIW 8
Db	1 GYWXXXW 7
RESULT 5	
ABP53968	
ID	ABP53968 standard; peptide; 10 AA.
XX	
AC	ABP53968;
XX	
DT	09-JAN-2003 (first entry)
XX	
DE	VEGFR-3 binding peptide SEQ ID NO:73.
XX	
KW	Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW	angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW	cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW	vulnary; cell surface receptor; cancer; neovascularisation;
KW	liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW	diabetes; PDGF; platelet derived growth factor.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 5. .7 /note= "X is any amino acid"
FT	
FT	Misc-difference 9 /note= "X is any amino acid"
FT	
XX	
PN	WO200257299-A2.
XX	
PD	25-JUL-2002.
XX	
PF	16-JAN-2002; 2002WO-IB000099.
XX	
PR	17-JAN-2001; 2001US-0262476P.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(LICN ) LICENTIA LTD.
XX	
PI	Alitalo K, Koivunen E, Kubo H;
XX	
DR	WPI; 2002-691521/74.
XX	
PT	New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT	diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT	such as cancer and diseases of neovascularization.
XX	
PS	Disclosure; Page 147; 149pp; English.
XX	
CC	The present invention describes an isolated peptide (I) that binds to and
CC	inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC	have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC	antidiabetic and vulnary activities, and can be used in gene therapy.
CC	Compositions and methods from the present invention are useful for
CC	diagnosing, evaluating and treating disorders mediated by the activity of
CC	the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC	liver, spleen, kidney, lymph node, small intestine, blood cells,
CC	pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,

CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a VEGFR-3 binding peptide, which is given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 58.9%; Score 33; DB 5; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 GYWLTIW 8  
Db 2 GYWXXW 8  
  
RESULT 6  
AAAY76794  
ID AAAY76794 standard; peptide; 7 AA.  
XX  
AC AAAY76794;  
XX  
DT 20-APR-2000 (first entry)  
XX  
DE Somatostatin analogue peptide 3181.  
XX  
KW Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 3  
FT /note= "D-form residue"  
FT Modified-site 7  
FT /note= "Trp-NH2"  
XX  
PN WO9965508-A1.  
XX  
PD 23-DEC-1999.  
XX  
PF 15-JUN-1999; 99WO-IL000329.  
XX  
PR 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
XX  
PA (PEPT-) PEPTOR LTD.  
XX  
PI Hornik V, Afargan MM, Gellerman G;  
XX  
DR WPI; 2000-136888/12.  
XX  
PT Cyclized somatostatin analogs for inhibiting growth hormone secretion  
PT from anterior pituitary and as antiproliferative agents for the treatment  
PT of tumors.  
XX  
PS Example 11; Page 61; 82pp; English.  
XX  
CC This sequence represents a somatostatin analogue of the invention. The  
CC invention relates to a backbone cyclised somatostatin analogue that has  
CC one building unit containing a nitrogen atom of the peptide backbone  
CC connected to a bridging group comprising an amide, thioether, thioester  
CC or disulphide. At least one building unit is connected via a bridging  
CC group to form a cyclic structure with a moiety selected from a second  
CC building unit, side chain of or N-terminal amino acid residue. A  
CC composition containing the analogue may be used for preventing disorders  
CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
CC associated complications, gastrointestinal disorders, inflammatory

CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
CC analogue is used for imaging the existence of metastases. Somatostatin  
CC analogues can be used for the treatment patients with hormone-secreting  
CC and hormone-dependent tumours. They reduce diarrhoea through the  
CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
CC effect on intestinal secretion. Somatostatin analogues selective to type  
CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
CC and restenosis. The analogues are metabolically stable, selective in  
CC their in-vivo activities and safe  
XX  
SQ Sequence 7 AA;  
  
Query Match 57.1%; Score 32; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 GYWLTIW 8  
Db 1 GYWKVCW 7  
  
RESULT 7  
ABP53418  
ID ABP53418 standard; peptide; 7 AA.  
XX  
AC ABP53418;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Backbone cyclised somatostatin analogue PTR 3181.  
XX  
KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
KW somatotropin release inhibiting factor; somatostatin receptor subtype;  
KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;  
KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
KW pancreatitis; post-surgical pain.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminally modified with Fmoc  
(fluorenylmethoxycarbonyl)"  
FT Misc-difference 3  
FT /note= "D form residue"  
FT Modified-site 7  
FT /note= "amidated"  
XX  
PN US2002052315-A1.  
XX  
PD 02-MAY-2002.  
XX  
PF 13-DEC-2000; 2000US-00734583.  
XX  
PR 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
PR 15-JUN-1999; 99WO-IL000329.  
XX  
PA (HORN/) HORNIK V.  
PA (AFAR/) AFARGAN M M.  
PA (GELL/) GELLERMAN G.  
XX  
PI Hornik V, Afargan MM, Gellerman G;  
XX  
DR WPI; 2002-681319/73.  
XX  
PT New backbone cyclized somatostatin analogs are e.g. useful in the  
PT treatment of atherosclerosis, autoimmune diseases and cancers.  
XX





QY 2 GYWLTIW 8  
| | | | |  
Db 2 GYWWDTW 8

RESULT 10  
ADN64476  
ID ADN64476 standard; peptide; 9 AA.  
XX AC ADN64476;  
XX DT 01-JUL-2004 (first entry)  
XX DE HLA binding peptide #1076.  
XX KW cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;  
KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;  
KW prostate specific antigen; prostate specific membrane antigen;  
KW hepatitis B virus antigen; hepatitis C virus antigen;  
KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;  
KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;  
KW chondyloma acuminatum.  
XX OS Unidentified.  
XX PN WO2004031211-A2.  
XX PD 15-APR-2004.  
XX PF 03-OCT-2003; 2003WO-US031308.  
XX PR 03-OCT-2002; 2002US-0416207P.  
XX PR 08-OCT-2002; 2002US-0417269P.  
XX PA (EPIM-) EPIMMUNE INC.  
XX PI Sidney J, Southwood S, Sette A;  
XX WPI; 2004-347953/32.  
XX New composition of peptides and nucleic acids capable of binding Major  
PT Histocompatibility Complex molecules, useful for diagnosing, preventing  
PT or treating viral infections or cancer, such as prostate cancer,  
PT hepatitis B or AIDS.  
XX PS Claim 1; SEQ ID NO 1076; 186pp; English.  
XX The invention relates to a novel composition comprising one or more  
CC peptides or nucleic acids encoding an HLA binding peptide. The  
CC composition further comprises an HTL epitope. It also comprises a spacer  
CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides  
CC are incorporated as part of a liposome. The peptide is from an antigen  
CC selected from prostate specific antigen (PSA), prostate specific membrane  
CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)  
CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human  
CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),  
CC Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,  
CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein  
CC (TKP). The composition is useful for preventing or treating viral  
CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,  
CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyloma  
CC acuminatum. The composition is also be used for diagnosing such diseases.  
XX This sequence represents a peptide of the invention.  
SQ Sequence 9 AA;

Query Match 55.4%; Score 31; DB 8; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 WLTIW 8  
| : | : |  
Db 5 WVTWV 9

RESULT 11  
AAG95260  
ID AAG95260 standard; peptide; 10 AA.  
XX AC AAG95260;  
XX DT 18-SEP-2001 (first entry)  
XX DE Human complementary peptide, SEQ ID NO: 1454.  
XX KW Human; complementary peptide; ligand; drug discovery; drug design.  
XX OS Homo sapiens.  
XX PN WO200142277-A2.  
XX PD 14-JUN-2001.  
XX PF 13-DEC-2000; 2000WO-GB004776.  
XX PR 13-DEC-1999; 99GB-00029464.  
XX PA (PROT-) PROTEOM LTD.  
XX PI Roberts GW, Heal JR;  
XX WPI; 2001-408419/43.  
XX A set of peptide ligands consisting of specific complementary peptides to  
PT proteins encoded by genes of the human genome, useful in an assay for  
PT screening and identifying of one or more novel peptides which are drug  
PT candidates or pro-drugs.  
XX PS Example 4; Page 250; 646pp; English.  
XX The invention relates to a set of complementary peptide ligands generated  
CC from the human genome. The complementary peptides interact with their  
CC relevant target proteins encoded in the human genome. They can be used as  
CC reagents in drug discovery and as lead ligands to facilitate drug design  
CC and development. The present sequence is a complementary peptide provided  
CC in the specification  
XX SQ Sequence 10 AA;

Query Match 55.4%; Score 31; DB 4; Length 10;  
Best Local Similarity 62.5%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | | | |  
Db 1 GVWLTVIG 8

RESULT 12  
AAR14709  
ID AAR14709 standard; peptide; 10 AA.  
XX AC AAR14709;  
XX DT 25-MAR-2003 (revised)  
DT 24-JAN-1992 (first entry)  
XX DE Labaditin.  
XX KW Cyclic; immunoglobulin; autoimmune disease.  
XX OS Jatropa multifida.  
XX PN WO9116345-A.  
XX PD 31-OCT-1991.

XX 23-APR-1990; 90US-00512796.  
PF  
XX  
PR 23-APR-1990; 90US-00512796.  
XX  
XX (UYUT-) RIJKSUNIV UTRECHT.  
PA  
XX Labadie RP;  
PI  
XX  
DR WPI; 1991-339755/46.  
XX  
PT New cyclic peptide(s) e.g. labaditin, having IgG binding properties -  
PT used for IgG binding in mammals including humans and for treating  
PT inflammatory diseases including rheumatic and auto:immune diseases.  
XX  
XX  
PS Claim 11; Page 12; 15pp; English.  
XX  
CC The peptide is isolated from plants of the Euphorbiaceae family (see FEBS  
CC Letters 256, 1-2, 1989). It selectively inhibits the classical activation  
CC pathway of the complement system by binding to IgG. It can be used to  
CC treat autoimmune disorders e.g. rheu- matic and other inflammatory  
CC disorders, and immuno-complex-related diseases, e.g. extrinsic allergic  
CC alveolitis. It may also be used to isolate IgG from blood plasma or serum  
CC to reduce the level of IgG, or as immunoassay reagent to determine IgG  
CC levels in body fluids. See also AAR14710. (Updated on 25-MAR-2003 to  
CC correct PA field.)  
XX  
SQ Sequence 10 AA;  
  
Query Match 54.5%; Score 30.5; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
  
QY 2 GYWLTIWG 9  
| | | | |  
Db 2 GVN-TVWG 8  
  
RESULT 13  
AAU02369  
ID AAU02369 standard; peptide; 9 AA.  
XX  
AC AAU02369;  
XX  
XX 29-AUG-2001 (first entry)  
XX  
DE HLA binding TADG-16 peptide #145.  
XX  
KW Human; extracellular serine protease; tumour antigen derived gene-16;  
KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;  
KW prostate cancer; HLA type.  
XX  
OS Homo sapiens.  
XX  
PN WO200127257-A1.  
XX  
PD 19-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028558.  
XX  
PR 14-OCT-1999; 99US-00418527.  
XX  
PA (UYAR-) UNIV ARKANSAS.  
XX  
PI O'Brien TJ, Underwood LJ, Shigemasa K;  
XX  
DR WPI; 2001-273769/28.  
XX  
PT New tumor antigen-derived gene-16 protein, useful for diagnosis and  
PT treatment of ovarian, breast, lung, colon and prostate cancer.  
XX  
PS Example 8; Page 55; 124pp; English.  
XX

CC AAU02225-AAU02384 represent TADG-16 peptides which are tested for their  
CC binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA  
CC A24, HLA B7, HLA B8, HLA B2702, and HLA B4403. Tumour antigen derived  
CC gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular  
CC serine protease. TADG-16 is expressed in normal ovaries and testes and in  
CC certain ovarian carcinomas. TADG-16 contains the conserved catalytic  
CC triad, His-Asp-Ser, and a signal secretion sequence characteristic of the  
CC serine protease family. An antisense oligonucleotide having a  
CC complementary sequence to the TADG-16 nucleic acid is useful for treating  
CC various cancers, including ovarian, breast, lung, colon and prostate. The  
CC TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16  
CC are useful for the diagnosis of cancer. TADG-16 protein or its fragments  
XX are useful for vaccinating an individual against TADG-16  
SQ Sequence 9 AA;  
  
Query Match 53.6%; Score 30; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 WLTIWG 9  
| | | | |  
Db 3 WVTGWG 8  
  
RESULT 14  
AAU02282  
ID AAU02282 standard; peptide; 9 AA.  
XX  
AC AAU02282;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE HLA binding TADG-16 peptide #58.  
XX  
KW Human; extracellular serine protease; tumour antigen derived gene-16;  
KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;  
KW prostate cancer; HLA type.  
XX  
OS Homo sapiens.  
XX  
PN WO200127257-A1.  
XX  
PD 19-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028558.  
XX  
PR 14-OCT-1999; 99US-00418527.  
XX  
PA (UYAR-) UNIV ARKANSAS.  
XX  
PI O'Brien TJ, Underwood LJ, Shigemasa K;  
XX  
DR WPI; 2001-273769/28.  
XX  
PT New tumor antigen-derived gene-16 protein, useful for diagnosis and  
PT treatment of ovarian, breast, lung, colon and prostate cancer.  
XX  
PS Example 8; Page 53; 124pp; English.  
XX  
CC AAU02225-AAU02384 represent TADG-16 peptides which are tested for their  
CC binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA  
CC A24, HLA B7, HLA B8, HLA B2702, and HLA B4403. Tumour antigen derived  
CC gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular  
CC serine protease. TADG-16 is expressed in normal ovaries and testes and in  
CC certain ovarian carcinomas. TADG-16 contains the conserved catalytic  
CC triad, His-Asp-Ser, and a signal secretion sequence characteristic of the  
CC serine protease family. An antisense oligonucleotide having a  
CC complementary sequence to the TADG-16 nucleic acid is useful for treating  
CC various cancers, including ovarian, breast, lung, colon and prostate. The  
CC TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16  
CC are useful for the diagnosis of cancer. TADG-16 protein or its fragments  
XX are useful for vaccinating an individual against TADG-16

XXSQSequence 9 AA;

Query Match  
Best Local Similarity 53.6%; Score 30; DB 4; Length 9;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY4 WLTIMG 9  
|.|||

Db1 WVTGWG 6

Query Match  
Best Local Similarity 53.6%; Score 30; DB 4; Length 10;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY2 GYWLTIW 8  
|||

Db1 GWSAKW 7

Search completed: December 29, 2004, 21:35:31  
Job time : 97.3333 secs

RESULT 15  
AAB99759  
ID AAB99759 standard; peptide; 10 AA.  
XX  
AC AAB99759;  
XX  
DT 21-SEP-2001 (first entry)  
XX  
DE Rhesus D antibody binding peptide SEQ ID NO:4.  
XX  
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP;  
KW idiopathic thrombocytopaenic purpura; immunoglobulin.  
XX  
OS Homo sapiens.  
XX  
PN EP1106625-A1.  
XX  
PD 13-JUN-2001.  
XX  
PF 17-NOV-1999; 99EP-00122858.  
XX  
PR 17-NOV-1999; 99EP-00122858.  
XX  
PA (ZLBB-) ZLB BIOPLASMA AG.  
XX  
PI Miescher S, Hofmann A, Fisch I;  
XX  
DR WPI; 2001-383568/41.  
XX  
PT Novel peptides capable of binding Rhesus D antibodies are used to  
PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the  
PT newborn (HDN).  
XX  
PS Claim 1; Page 12; 19pp; English.  
XX  
CC The present sequence represents a peptide capable of binding Rhesus D  
CC antibodies (I). Also described in the present invention are: (1) a  
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
CC (II) operably linked to an expression control system; (3) a cell (IV)  
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
CC peptides having immunologic properties of Rhesus D protein epitopes  
CC comprising subjecting an antibody/antibody fragment recognising an  
CC epitope of Rhesus D protein to several panning rounds with a phage  
CC display library, and identifying immunogenic peptide sequences which are  
CC mimotopes which differ in their amino acid sequence from the amino acid  
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
CC newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the  
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
CC with foreign erythrocytes thereby avoiding the risk of transmission of  
CC viral diseases like AIDS and hepatitis B  
XX  
SQ Sequence 10 AA;



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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds  
(without alignments)  
28.022 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	51.8	7	4	US-09-069-827A-94
2	29	51.8	9	4	US-09-311-784A-348
3	29	51.8	10	2	US-08-735-253-8
4	29	51.8	10	2	US-08-735-253-13
5	28	50.0	8	3	US-09-315-304B-1649
6	28	50.0	10	4	US-09-125-641-3
7	27.5	49.1	6	1	US-08-191-571-12
8	27.5	49.1	6	5	PCT-US95-00296-12
9	27	48.2	8	3	US-08-586-670A-17
10	27	48.2	8	3	US-09-082-279B-1495
11	27	48.2	8	4	US-09-834-784-1495
12	27	48.2	8	4	US-09-350-641C-1650
13	27	48.2	10	3	US-09-315-304B-1587
14	27	48.2	10	4	US-09-350-325-47
15	27	48.2	10	4	US-09-350-641C-1587
16	27	48.2	10	4	US-09-239-043D-2474
17	27	48.2	10	4	US-09-620-091-28
18	26	46.4	5	1	US-08-353-400-27
19	26	46.4	6	1	US-08-415-099A-3
20	26	46.4	8	1	US-08-415-099A-4
21	26	46.4	8	3	US-08-467-472C-5
22	26	46.4	8	3	US-08-467-472C-6
23	26	46.4	8	3	US-09-082-279B-1500
24	26	46.4	8	3	US-09-384-061-5
25	26	46.4	8	3	US-09-384-061-6
26	26	46.4	8	4	US-09-834-784-1500
27	26	46.4	8	4	US-08-632-444B-9

28	26	46.4	8	4	US-09-350-641C-1655	Sequence 1655, Ap
29	26	46.4	8	4	US-09-852-870A-5	Sequence 5, Appli
30	26	46.4	9	1	US-08-024-253-18	Sequence 18, Appl
31	26	46.4	9	3	US-08-985-526-13	Sequence 13, Appl
32	26	46.4	10	4	US-08-632-444B-10	Sequence 10, Appl
33	26	46.4	10	4	US-09-852-870A-6	Sequence 6, Appli
34	26	46.4	10	4	US-09-620-091-41	Sequence 41, Appl
35	25.5	45.5	8	1	US-08-191-571-21	Sequence 21, Appl
36	25.5	45.5	8	5	PCT-US95-00296-21	Sequence 21, Appl
37	25	44.6	5	4	US-09-155-106-1	Sequence 1, Appli
38	25	44.6	6	2	US-08-660-747-56	Sequence 56, Appl
39	25	44.6	8	4	US-09-125-641-1	Sequence 1, Appli
40	25	44.6	8	4	US-09-125-641-2	Sequence 2, Appli
41	25	44.6	9	4	US-09-125-641-29	Sequence 29, Appl
42	25	44.6	10	1	US-08-208-886C-83	Sequence 83, Appl
43	25	44.6	10	1	US-08-208-886C-87	Sequence 87, Appl
44	25	44.6	10	1	US-08-704-744-85	Sequence 85, Appl
45	25	44.6	10	1	US-08-704-744-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1  
US-09-069-827A-94  
; Sequence 94, Application US/09069827A  
; Patent No. 6617114  
; GENERAL INFORMATION:  
; APPLICANT: FOWLKES, Dana M  
; KAY, Brian K  
; FRELINGER, Jeffrey A  
; HYDE-DERUYSCHE, Robin P  
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING  
; COMPLEMENTARY COMBINATORIAL LIBRARIES  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 624 Ninth Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/069,827A  
; APPLICATION NUMBER: 09/069,827A  
; FILING DATE: 30-Apr-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/050,359  
; FILING DATE: 31-MAR-1998  
; APPLICATION NUMBER: PCT/US97/19638  
; FILING DATE: 31-OCT-1997  
; APPLICATION NUMBER: US 08/740,671  
; FILING DATE: 31-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOWLKES=4C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:



US-09-069-827A-94

Query Match 51.8%; Score 29; DB 4; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 3 YWLTIWG 9  
Db 1 YWPDWG 7  
  
RESULT 2  
US-09-311-784A-348  
; Sequence 348, Application US/09311784A  
; Patent No. 6534482  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)  
US-09-311-784A-348

Query Match 51.8%; Score 29; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTIWG 9  
Db 4 LTVWG 8

RESULT 3  
US-08-735-253-8  
; Sequence 8, Application US/08735253  
; Patent No. 5942491  
; GENERAL INFORMATION:  
; APPLICANT: Root-Bernstein, Robert S.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Arthritis  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.  
; STREET: 180 N. Stetson  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/735,253  
; FILING DATE:

; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5942491thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: MIC3302P0010US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 616-5400  
; TELEFAX: (3120 616-5460  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-735-253-8  
  
Query Match 51.8%; Score 29; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 YWLTIWG 9  
Db 1 FWRFLWG 7

RESULT 4  
US-08-735-253-13  
; Sequence 13, Application US/08735253  
; Patent No. 5942491  
; GENERAL INFORMATION:  
; APPLICANT: Root-Bernstein, Robert S.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Arthritis  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.  
; STREET: 180 N. Stetson  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/735,253  
; FILING DATE:

; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5942491thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: MIC3302P0010US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 616-5400  
; TELEFAX: (3120 616-5460  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-735-253-13

Query Match 51.8%; Score 29; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTIWG 9  
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Db      1 FWRFLWG 7

RESULT 5
US-09-315-304B-1649
; Sequence 1649, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1649
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-09-315-304B-1649

Query Match      50.0%; Score 28; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 WLTWNG 9
      | : : | |
Db      1 WNSLWG 6

RESULT 6
US-09-125-641-3
; Sequence 3, Application US/09125641
; Patent No. 6610297
; GENERAL INFORMATION:
; APPLICANT: Kricek, Franz
; APPLICANT: Stadler, Beda
; TITLE OF INVENTION: Peptide Immunogens For Vaccination
; TITLE OF INVENTION: Against and Treatment of Allergy
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6610297artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,641
; FILING DATE: 21-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/01013
; FILING DATE: 28-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9604412.8
; FILING DATE: 01-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9617702.7
; FILING DATE: 22-AUG-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 4-900-9862/A/NFI/PCT
TELEPHONE: (908) 522-6923
TELEFAX: (908) 522-6923
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-09-125-641-3

Query Match      50.0%; Score 28; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWL 5
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Db      6 GYWL 9

RESULT 7
US-08-191-571-12
; Sequence 12, Application US/08191571
; Patent No. 5521156
; GENERAL INFORMATION:
; APPLICANT: Owen, Thomas J.
; APPLICANT: Kudlacz, Elizabeth M
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: P. O. Box 156300 2110 E. Galbraith Rd.
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: United States
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/191,571
; FILING DATE: 03-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-191-571-12

Query Match      49.1%; Score 27.5; DB 1; Length 6;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 3 YWLTWG 9  
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Db 1 YWLR-WG 6

RESULT 8  
PCT-US95-00296-12  
; Sequence 12, Application PC/TUS9500296  
; GENERAL INFORMATION:  
; APPLICANT: Merrell Dow Pharmaceuticals Inc.  
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marion Merrell Dow Inc.  
; STREET: 2110 East Galbraith Road, P.O. Box 156300  
; CITY: Cincinnati  
; STATE: OH  
; COUNTRY: USA  
; ZIP: 45215-6300  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00296  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Boudreaux, William R  
; REGISTRATION NUMBER: 35,796  
; REFERENCE/DOCKET NUMBER: M01718A WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 513-948-6566  
; TELEFAX: 513-948-7961 or 4681  
; TELEX: 214320  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
PCT-US95-00296-12

Query Match 49.1%; Score 27.5; DB 5; Length 6;  
Best Local Similarity 71.4%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 YWLTWG 9  
| | | | |  
Db 1 YWLR-WG 6

RESULT 9  
US-08-586-670A-17  
; Sequence 17, Application US/08586670A  
; Patent No. 6241965  
; GENERAL INFORMATION:  
; APPLICANT: McBride, William  
; APPLICANT: Dean, Richard T.  
; TITLE OF INVENTION: Somatostatin Derivatives  
; TITLE OF INVENTION: And their Radiolabeled Products  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 10 South Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/586,670A  
; FILING DATE: 22-APR-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6241965nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 92,385-DD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; TELEX: 910-221-5317  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1..2  
; OTHER INFORMATION: /label= Variant residues  
; OTHER INFORMATION: /note= "phe is in the D conformation and is  
; OTHER INFORMATION: linked to DTPA;  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1..4  
; OTHER INFORMATION: /label= Variant residues  
; OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa  
; OTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the  
; OTHER INFORMATION: D conformation;  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 7..8  
; OTHER INFORMATION: /label= Variant residues  
; OTHER INFORMATION: /note= "The carboxyl group of the C-terminal  
; OTHER INFORMATION: Thr is reduced to an alcohol;  
US-08-586-670A-17

Query Match 48.2%; Score 27; DB 3; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLT 6  
| | | | |  
Db 2 GYWKT 6

RESULT 10  
US-09-082-279B-1495  
; Sequence 1495, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1495  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
US-09-082-279B-1495

Query Match 48.2%; Score 27; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTWIG 9  
| : : |  
Db 1 WDSLWG 6

RESULT 11  
US-09-834-784-1495  
; Sequence 1495, Application US/09834784  
; Patent No. 6562787  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/834,784  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1495  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
US-09-834-784-1495

Query Match 48.2%; Score 27; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTWIG 9  
| : : |  
Db 1 WDSLWG 6

RESULT 12  
US-09-350-641C-1650  
; Sequence 1650, Application US/09350641C  
; Patent No. 6656906  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-067  
; CURRENT APPLICATION NUMBER: US/09/350,641C  
; CURRENT FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1650  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
US-09-350-641C-1650

Query Match 48.2%; Score 27; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTWIG 9  
| : : |  
Db 1 WDSLWG 6

RESULT 13  
US-09-315-304B-1587  
; Sequence 1587, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1587  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1587

Query Match 48.2%; Score 27; DB 3; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| : : |  
Db 1 GGWASLW 7

RESULT 14  
US-09-350-325-47  
; Sequence 47, Application US/09350325  
; Patent No. 6541020  
; GENERAL INFORMATION:  
; APPLICANT: Ding, S.  
; APPLICANT: Kang, M.  
; APPLICANT: Venetta, T.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF  
; TITLE OF INVENTION: THERAPEUTIC REAGENTS  
; FILE REFERENCE: 7872-062  
; CURRENT APPLICATION NUMBER: US/09/350,325  
; CURRENT FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 47  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: enhancer peptide  
US-09-350-325-47

Query Match 48.2%; Score 27; DB 4; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| : : |  
Db 1 GGWASLW 7

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RESULT 15
US-09-350-641C-1587
; Sequence 1587, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1587
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-1587
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Query Match      48.2%; Score 27; DB 4; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      2 GYWLTIW 8
      | | : |
Db      1 GGWASLW 7
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Search completed: December 29, 2004, 21:36:44  
Job time : 24.6667 secs



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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:36:53 ; Search time 82 Seconds  
(without alignments)  
43.869 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues 182644  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
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  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	96.4	10	13 US-10-046-922-34	Sequence 34, Appl
2	54	96.4	10	13 US-10-046-922-35	Sequence 35, Appl
3	33	58.9	7	13 US-10-046-922-67	Sequence 67, Appl
4	33	58.9	8	13 US-10-046-922-68	Sequence 68, Appl
5	33	58.9	10	13 US-10-046-922-73	Sequence 73, Appl
6	31	55.4	9	13 US-10-046-922-36	Sequence 36, Appl
7	31	55.4	10	10 US-09-572-404B-1454	Sequence 1454, Ap
8	30	53.6	10	15 US-10-462-452-707	Sequence 707, App
9	30	53.6	10	15 US-10-601-953-812	Sequence 812, App
10	30	53.6	10	16 US-10-322-266-708	Sequence 708, App
11	29	51.8	9	9 US-09-894-018-154	Sequence 154, App
12	29	51.8	9	14 US-10-133-210-8	Sequence 8, Appli
13	29	51.8	9	14 US-10-371-525-348	Sequence 348, App

14	29	51.8	9	14	US-10-371-069-348	Sequence 348, App
15	29	51.8	9	14	US-10-371-645-348	Sequence 348, App
16	29	51.8	9	14	US-10-371-260-348	Sequence 348, App
17	29	51.8	9	15	US-10-182-252A-180	Sequence 180, App
18	29	51.8	9	15	US-10-182-252A-181	Sequence 181, App
19	29	51.8	9	15	US-10-182-252A-305	Sequence 305, App
20	29	51.8	9	15	US-10-182-252A-792	Sequence 792, App
21	29	51.8	9	15	US-10-182-252A-793	Sequence 793, App
22	29	51.8	9	15	US-10-182-252A-837	Sequence 837, App
23	29	51.8	9	15	US-10-182-252A-838	Sequence 838, App
24	29	51.8	9	15	US-10-182-252A-1271	Sequence 1271, Ap
25	29	51.8	9	17	US-10-474-960A-154	Sequence 154, App
26	29	51.8	10	8	US-08-821-739A-92	Sequence 92, Appl
27	29	51.8	10	14	US-10-133-210-7	Sequence 7, Appli
28	29	51.8	10	14	US-10-133-210-40	Sequence 40, Appl
29	29	51.8	10	14	US-10-133-210-70	Sequence 70, Appl
30	29	51.8	10	14	US-10-200-708-355	Sequence 355, App
31	29	51.8	10	14	US-10-200-708-581	Sequence 581, App
32	28	50.0	10	10	US-09-793-451-69	Sequence 69, Appl
33	28	50.0	10	14	US-10-050-902-181	Sequence 181, App
34	28	50.0	10	14	US-10-050-898-181	Sequence 181, App
35	28	50.0	10	14	US-10-283-722-69	Sequence 69, Appl
36	28	50.0	10	14	US-10-283-903-69	Sequence 69, Appl
37	28	50.0	10	15	US-10-617-876-33	Sequence 33, Appl
38	27	48.2	8	14	US-10-351-641-1650	Sequence 1650, Ap
39	27	48.2	9	15	US-10-239-656-11	Sequence 11, Appl
40	27	48.2	10	14	US-10-347-562-47	Sequence 47, Appl
41	27	48.2	10	14	US-10-351-641-1587	Sequence 1587, Ap
42	27	48.2	10	15	US-10-239-656-34	Sequence 34, Appl
43	27	48.2	10	15	US-10-239-656-44	Sequence 44, Appl
44	27	48.2	10	16	US-10-327-598-450	Sequence 450, App
45	26	46.4	7	9	US-09-884-767A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; TYPE: PRT  
; LENGTH: 10  
; ORGANISM: isolated peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 96.4%; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9

Db 2 GYWLTIWG 9

RESULT 2  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
US-10-046-922-35

Query Match 96.4%; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
|||  
Db 2 GYWLTIWG 9

RESULT 3  
US-10-046-922-67  
; Sequence 67, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X at position 4-6 is any amino acid  
US-10-046-922-67

Query Match 58.9%; Score 33; DB 13; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||  
Db 1 GYWXXXW 7

RESULT 4  
US-10-046-922-68  
; Sequence 68, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922

; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 68  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-68

Query Match 58.9%; Score 33; DB 13; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||  
Db 1 GYWXXXW 7

RESULT 5  
US-10-046-922-73  
; Sequence 73, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 73  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: peptide library  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (5)..(7)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-73

Query Match 58.9%; Score 33; DB 13; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||  
Db 2 GYWXXXW 8

RESULT 6  
US-10-046-922-36  
; Sequence 36, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15

; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: peptide  
US-10-046-922-36

Query Match 55.4%; Score 31; DB 13; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GWLTIW 8  
||| |  
Db 2 GYWDTW 8

RESULT 7  
US-09-572-404B-1454  
; Sequence 1454, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1454  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in P2RY5 at 139-148 and may interact with Sequen  
US-09-572-404B-1454

Query Match 55.4%; Score 31; DB 10; Length 10;  
Best Local Similarity 62.5%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GWLTIWG 9  
|||| |  
Db 1 GWLTVIG 8

RESULT 8  
US-10-462-452-707  
; Sequence 707, Application US/10462452  
; Publication No. US20040037809A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven  
; APPLICANT: El Shafy, Mohammed Abd  
; APPLICANT: Gupta, Malini  
; APPLICANT: de Meireles, Jorge  
; TITLE OF INVENTION: Compositions and Methods for Enhanced  
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta  
; FILE REFERENCE: 02-02US  
; CURRENT APPLICATION NUMBER: US/10/462,452  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: 60/393,066  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 790  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 707  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-462-452-707

Query Match 53.6%; Score 30; DB 15; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 3 YWLTIW 8  
|| : |  
Db 5 YWANLW 10

RESULT 9  
US-10-601-953-812  
; Sequence 812, Application US/10601953  
; Publication No. US20040077540A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven C.  
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial  
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of  
; TITLE OF INVENTION: Therapeutic Compounds  
; FILE REFERENCE: 02-03US  
; CURRENT APPLICATION NUMBER: US/10/601,953  
; CURRENT FILING DATE: 2003-06-24  
; PRIOR APPLICATION NUMBER: 60/392,512  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 812  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-601-953-812

Query Match 53.6%; Score 30; DB 15; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YWLTIW 8  
|| : |  
Db 5 YWANLW 10

RESULT 10  
US-10-322-266-708  
; Sequence 708, Application US/10322266  
; Publication No. US20040115135A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven C.  
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide  
; TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity  
; FILE REFERENCE: NPCI0567  
; CURRENT APPLICATION NUMBER: US/10/322,266  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 797  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 708  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-322-266-708

Query Match 53.6%; Score 30; DB 16; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YWLTIW 8  
|| : |  
Db 5 YWANLW 10

RESULT 11  
US-09-894-018-154  
; Sequence 154, Application US/09894018

Patent No. US20020119127A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Deniaw  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING  
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY  
; FILE REFERENCE: 39963-20033.00  
; CURRENT APPLICATION NUMBER: US/09/894,018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: PCT/US00/35568  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 154  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Transgenic mouse  
US-09-894-018-154

Query Match 51.8%; Score 29; DB 9; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTIWG 9  
||:||  
Db 4 LTVWG 8

RESULT 12  
US-10-133-210-8  
; Sequence 8, Application US/10133210  
; Publication No. US20030103964A1  
; GENERAL INFORMATION:  
; APPLICANT: DeLisi, Charles  
; APPLICANT: Berzofsky, Jay  
; APPLICANT: Gulukota, Kamalakar  
; APPLICANT: Vaccaro, Dennis  
; APPLICANT: Weng, Zhiping  
; APPLICANT: Zhang, Chao  
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND  
; TITLE OF INVENTION: COMPOSITIONS THEREOF  
; FILE REFERENCE: BU-035AX  
; CURRENT APPLICATION NUMBER: US/10/133,210  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 281  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-133-210-8

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTIWG 9  
||:||  
Db 4 LTVWG 8

RESULT 13

US-10-371-525-348  
; Sequence 348, Application US/10371525  
; Publication No. US20030203869A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/10/371,525  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 09/311,784  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)  
US-10-371-525-348

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTIWG 9  
||:||  
Db 4 LTVWG 8

RESULT 14  
US-10-371-069-348  
; Sequence 348, Application US/10371069  
; Publication No. US20030216342A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE Inc.  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.10  
; CURRENT APPLICATION NUMBER: US/10/371,069  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 09/078,904  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)  
US-10-371-069-348

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
||:|

Db 4 LTVWG 8

RESULT 15  
US-10-371-645-348  
; Sequence 348, Application US/10371645  
; Publication No. US20030216343A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE Inc.  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; FILE REFERENCE: 39963-20022.11  
; CURRENT APPLICATION NUMBER: US/10/371,645  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: US 09/078,904  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)  
US-10-371-645-348

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
||:|

Db 4 LTVWG 8

Search completed: December 29, 2004, 22:01:39  
Job time : 83 secs



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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:30:17 ; Search time 19 Seconds  
(without alignments)  
50.640 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	42.9	10	S71868	glutathione transf
2	22	39.3	7	PT0586	T-cell receptor be
3	22	39.3	10	T17075	cytochrome-c oxida
4	20	35.7	5	JH0253	gut pentapeptide -
5	19	33.9	9	PT0324	Ig heavy chain CRD
6	19	33.9	10	PT0289	Ig heavy chain CRD
7	18	32.1	8	JS0315	leucokinin V - Mad
8	18	32.1	10	PT0230	Ig heavy chain CDR
9	18	32.1	10	F33932	Ig mu chain J regi
10	17	30.4	4	B53284	T-cell receptor be
11	17	30.4	6	PT0629	T-cell receptor be
12	17	30.4	6	PT0637	T-cell receptor be
13	17	30.4	6	A61068	locustakinin - mig
14	17	30.4	7	PT0628	T-cell receptor be
15	17	30.4	7	PT0642	T-cell receptor be
16	17	30.4	7	PT0722	T-cell receptor be
17	17	30.4	7	PT0728	T-cell receptor be
18	17	30.4	7	PX0008	glucuronosyltransf
19	17	30.4	7	B48394	major fat-globule
20	17	30.4	7	PD0029	pev-kinin I - pena
21	17	30.4	7	S57274	triacylglycerol li
22	17	30.4	7	S33244	neuromodulatory pe
23	17	30.4	7	S33245	neuromodulatory pe
24	17	30.4	7	S33246	neuromodulatory pe
25	17	30.4	8	PT0724	T-cell receptor be
26	17	30.4	8	JS0316	leucokinin VII - Ma
27	17	30.4	8	JS0317	leucokinin VII - M
28	17	30.4	8	JS0318	leucokinin VIII -
29	17	30.4	8	A31570	angiotensin-conver

30	17	30.4	9	2	A24244	adipokinetic hormo
31	17	30.4	9	2	PT0634	T-cell receptor be
32	17	30.4	9	2	PT0562	T-cell receptor be
33	17	30.4	9	2	A60522	sperm-activating p
34	17	30.4	10	2	B33995	hypotrehalosemic h
35	17	30.4	10	2	S08997	hypertrehalosemic
36	17	30.4	10	2	A60421	hypertrehalosemic
37	17	30.4	10	2	S08998	hypertrehalosemic
38	17	30.4	10	2	A26381	hypertrehalosemic
39	17	30.4	10	2	JC1416	hypertrehalosemic
40	17	30.4	10	2	S09138	hypertrehalosemic
41	17	30.4	10	2	A31571	hypertrehalosemic/
42	17	30.4	10	2	A49187	gonadotropin-relea
43	17	30.4	10	2	PH1344	Ig heavy chain DJ
44	17	30.4	10	2	PH0923	T-cell receptor be
45	17	30.4	10	2	A40753	aldehyde ferredoxi

ALIGNMENTS

RESULT 1

S71868

glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)

N;Alternate names: glutathione S-transferase class mu 4

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004

C;Accession: S71868

R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospra

A;Reference number: S71864; MUID:96332484; PMID:8760377

A;Accession: S71868

A;Molecule type: protein

A;Residues: 1-10 <ROU>

A;Cross-references: UNIPROT:Q7M3E8

C;Comment: At least five species-independent classes of cytosolic glutathion transferase

s mitochondrial form are known.

C;Complex: dimer

C;Function:

A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v

A;Pathway: detoxification; xenobiotics metabolism

A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism

es of damage

C;Superfamily: glutathione transferase

C;Keywords: dimer; transferase

Query Match 42.9%; Score 24; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYW 4

|||

Db 4 GYW 6

RESULT 2

PT0586

T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0586; PT0592

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0586

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)

C;Keywords: T-cell receptor

Query Match 39.3%; Score 22; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9  
    :| | |  
Db 3 SIWG 6

RESULT 3  
Tl17075  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)  
C;Species: mitochondrion Chamaeleo fischeri  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: Tl17075  
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
J. Mol. Evol. 44, 660-674, 1997  
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene  
A;Reference number: Z18674; MUID:97315309; PMID:9169559  
A;Accession: Tl17075  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-10 <MAC>  
A;Cross-references: UNIPROT:O79912; EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAC622  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 39.3%; Score 22; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 WLTIW 8  
    | | |  
Db 2 WLLRW 6

RESULT 4  
JH0253  
gut pentapeptide - Japanese eel  
C;Species: Anguilla japonica (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755  
A;Accession: JH0253  
A;Molecule type: protein  
A;Residues: 1-5 <UES>  
A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 35.7%; Score 20; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4  
    | : |  
Db 1 GFW 3

RESULT 5  
PT0324  
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0324  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0324  
A;Molecule type: DNA  
A;Residues: 1-9 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 19; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
    | | : |  
Db 3 GYGESYW 9

RESULT 6  
PT0289  
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0289  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0289  
A;Molecule type: DNA  
A;Residues: 1-10 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 19; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 3e+03;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIWG 9  
    | : : |  
Db 4 WISMGG 9

RESULT 7  
JS0315  
leucokinin V - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: JS0315  
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 27-30, 1987  
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic I  
A;Reference number: JS0315  
A;Accession: JS0315  
A;Molecule type: protein  
A;Residues: 1-8 <HOL>  
A;Cross-references: UNIPROT:P19987  
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile acti  
C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.1%; Score 18; DB 2; Length 8;  
Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
    | : | |  
Db 1 GSGFSSWG 8

RESULT 8  
PT0230  
Ig heavy chain CDR3 region (clone 1-118A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0230  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0230  
A;Molecule type: DNA  
A;Residues: 1-10 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 32.1%; Score 18; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
|||  
Db 3 ITIFG 7

RESULT 9  
F33932  
Ig mu chain J region (E7) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 09-Jul-2004  
C;Accession: F33932  
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l  
A;Reference number: A33932; MUID:89282823; PMID:2499887  
A;Accession: F33932  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-10 <BAC>  
A;Cross-references: UNIPROT:Q99NG4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q1; UNIP  
PROT:Q9DCD9; UNIPROT:Q924R0; UNIPROT:Q8K172; UNIPROT:Q99LA6; UNIPROT:Q91X92; GB:M27106  
C;Keywords: immunoglobulin

Query Match 32.1%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YW 4  
||  
Db 4 YW 5

RESULT 10  
B53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C;Accession: B53284  
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A;Title: Evolutionarily conserved organization and sequences of germline diversity and j  
A;Reference number: A53284; MUID:91342695; PMID:1678859  
A;Accession: B53284  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-4 <HAR>  
A;Cross-references: GB:S60737; NID:G2333916; PIDN:AAB19518.1; PID:G2333918  
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)  
C;Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 WG 9  
||  
Db 2 WG 3

RESULT 11  
PT0629  
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0629; PT0528  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0629  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH  
A;Accession: PT0528  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FE2>  
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB  
C;Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 WG 9  
||  
Db 5 WG 6

RESULT 12  
PT0637  
T-cell receptor beta chain V-D-J region (111-1K) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0637  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0637  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 WG 9  
||  
Db 5 WG 6

RESULT 13  
A61068  
locustakinin - migratory locust  
C;Species: Locusta migratoria (migratory locust)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: A61068  
R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.X.; De Loof, A.  
Regul. Pept. 37, 49-57, 1992  
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, prin  
A;Reference number: A61068; MUID:92262851; PMID:1585017  
A;Accession: A61068  
A;Molecule type: protein  
A;Residues: 1-6 <SCH>  
A;Cross-references: UNIPROT:P41491  
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide

F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.4%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WG 9  
||  
Db 5 WG 6

RESULT 14

PT0628  
T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0628  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0628  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WG 9  
||  
Db 6 WG 7

RESULT 15

PT0642  
T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0642  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0642  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WG 9  
||  
Db 5 WG 6



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OM protein - protein search, using sw model  
Run on: December 29, 2004, 21:27:57 ; Search time 100 Seconds  
(without alignments)  
57.537 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.5	54.5	10	1 LABA JATMU	P13270 jatropha mu
2	27	48.2	10	2 Q8SHF6	Q8shf6 chamaeleo m
3	26	46.4	8	2 Q70Y57	Q70y57 fuerstia af
4	26	46.4	8	2 CAD45547	Cad45547 fuerstia
5	24	42.9	10	2 Q7M3E8	Q7m3e8 sus scrofa
6	24	42.9	10	2 Q8SHN1	Q8shn1 bradypodion
7	24	42.9	10	2 Q6JL97	Q6jl97 neisseria g
8	24	42.9	10	2 AAS16521	Aas16521 neisseria
9	23.5	42.0	9	2 Q85DB0	Q85db0 lepitemur s
10	23.5	42.0	9	2 Q85DB8	Q85db8 lepitemur e
11	23.5	42.0	9	2 Q94NA9	Q94na9 daubentonla
12	23.5	42.0	9	2 Q94NB0	Q94nb0 microcebus
13	23.5	42.0	9	2 Q94NB1	Q94nb1 microcebus
14	23.5	42.0	9	2 Q94NB2	Q94nb2 microcebus
15	23.5	42.0	9	2 Q94XE6	Q94xe6 tectocoris
16	23	41.1	10	2 Q8SHC6	Q8shc6 furcifer be
17	22	39.3	10	2 Q79912	Q79912 chamaeleo f
18	22	39.3	10	2 Q9G697	Q9g697 chamaeleo d
19	22	39.3	10	2 Q8SH83	Q8sh83 brookesia t
20	22	39.3	10	2 Q8SH85	Q8sh85 brookesia t
21	22	39.3	10	2 Q8SH88	Q8sh88 brookesia t
22	22	39.3	10	2 Q8SH90	Q8sh90 brookesia s
23	22	39.3	10	2 Q8SH96	Q8sh96 brookesia p
24	22	39.3	10	2 Q8SHA2	Q8sha2 brookesia b
25	22	39.3	10	2 Q8SHA5	Q8sha5 brookesia a
26	22	39.3	10	2 Q8SHC9	Q8shc9 furcifer ba
27	22	39.3	10	2 Q8SHD2	Q8shd2 chamaeleo w
28	22	39.3	10	2 Q8SHD5	Q8shd5 chamaeleo s
29	22	39.3	10	2 Q8SHD8	Q8shd8 chamaeleo r
30	22	39.3	10	2 Q8SHE1	Q8she1 chamaeleo q
31	22	39.3	10	2 Q8SHE4	Q8she4 chamaeleo q

32	22	39.3	10	2 Q8SHE7	Q8she7 chamaeleo p
33	22	39.3	10	2 Q8SHF3	Q8shf3 chamaeleo m
34	22	39.3	10	2 Q8SHF9	Q8shf9 chamaeleo j
35	22	39.3	10	2 Q8SHG5	Q8shg5 chamaeleo h
36	22	39.3	10	2 Q8SHG8	Q8shg8 chamaeleo g
37	22	39.3	10	2 Q8SHH1	Q8shh1 chamaeleo f
38	22	39.3	10	2 Q8SHH4	Q8shh4 chamaeleo f
39	22	39.3	10	2 Q8SHH7	Q8shh7 chamaeleo e
40	22	39.3	10	2 Q8SHI0	Q8shi0 chamaeleo d
41	22	39.3	10	2 Q8SHI3	Q8shi3 chamaeleo c
42	22	39.3	10	2 Q8SHI6	Q8shi6 chamaeleo c
43	22	39.3	10	2 Q8SHI9	Q8shi9 chamaeleo c
44	22	39.3	10	2 Q8SHJ2	Q8shj2 chamaeleo a
45	22	39.3	10	2 Q8SHJ5	Q8shj5 calumma par

ALIGNMENTS

RESULT 1  
LABA JATMU  
ID LABA JATMU STANDARD; PRT; 10 AA.  
AC P13270;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Labaditin.  
OS Jatropha multifida (Physic nut).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophae;  
OC Jatropha.  
OX NCBI\_TaxID=3996;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Latex;  
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;  
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha  
multifida L. (Euphorbiaceae). Isolation and sequence determination by  
RT means of two-dimensional NMR.";  
RL FEBS Lett. 256:91-96(1989).  
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the  
CC classical pathway of complement activation in vitro. Activity  
CC seems to be based on an interaction with C1.  
CC -!- PTM: This is a cyclic peptide.  
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine  
CC for treatment of infected wounds, skins infections and scabies.  
KW Direct protein sequencing.  
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 54.5%; Score 30.5; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 2 GYWLTWIG 9  
| | | | |  
Db 2 GYW-TVWG 8

RESULT 2  
Q8SHF6  
ID Q8SHF6 PRELIMINARY; PRT; 10 AA.  
AC Q8SHF6;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Chamaeleo melleri (Meller's chameleon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.  
OX NCBI\_TaxID=179915;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169767; PubMed=12182400;
RA Townsend T., Larson A.;
RT "Molecular phylogenetics and mitochondrial genomic evolution in the
RT chamaeleonidae (Reptilia, Squamata).";
RL Mol. Phylogenet. Evol. 23:22-36(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448755; AAL90547.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1276 MW; 5E218E2733772727 CRC64;

Query Match 48.2%; Score 27; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIW 8
Db ||:|
2 WLLW 6

RESULT 3
Q70Y57 PRELIMINARY; PRT; 8 AA.
AC Q70Y57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rps16;
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 46.4%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
Db ||||
2 TIWG 5

RESULT 4
CAD45547 PRELIMINARY; PRT; 8 AA.
ID CAD45547
AC CAD45547;
DT 14-MAR-2004 (TrEMBLrel. 27, Created)
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
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GN RPS16.
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamials; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 46.4%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
Db ||||
2 TIWG 5

RESULT 5
Q7M3E8 PRELIMINARY; PRT; 10 AA.
ID Q7M3E8
AC Q7M3E8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE.
RA Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
RT "Characterization of pig liver glutathione S-transferases using HPLC-
RT electrospray-ionization mass spectrometry.";
RL Biochem. J. 317:879-884(1996).
DR PIR; S71868; S71868.
DR GO; GO:0004364; F:glutathione transferase activity; IEA.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1223 MW; 5E16395AB36B5877 CRC64;

Query Match 42.9%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4
Db |||
4 GYW 6

RESULT 6
Q8SHN1 PRELIMINARY; PRT; 10 AA.
ID Q8SHN1
AC Q8SHN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bradypodion tavetanum (Dwarf Fischer's chameleon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;  
OC Brachyopodion.  
OX NCBI\_TaxID=179888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22169767; PubMed=12182400;  
RA Townsend T., Larson A.;  
RT "Molecular phylogenetics and mitochondrial genomic evolution in the  
RT Chamaeleonidae (Reptilia, Squamata).";  
RL Mol. Phylogenet. Evol. 23:22-36(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Townsend T.M., Larson A.L.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF448730; AAL90472.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1327 MW; 5E2180C7336415B7 CRC64;  
  
Query Match 42.9%; Score 24; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 WLTW 8  
Db 2 WLSRW 6  
  
RESULT 7  
Q6JL97  
ID Q6JL97 PRELIMINARY; PRT; 10 AA.  
AC Q6JL97;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE NuOL (Fragment).  
GN Name=nuOL;  
OS Neisseria gonorrhoeae.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=485;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MS11;  
RX PubMed=15084227;  
RA Snyder L.A., Davies J.K., Saunders N.J.;  
RT "Microarray genotyping of key experimental strains of Neisseria  
RT gonorrhoeae reveals gene complement diversity and five new neisserial  
RT genes associated with Minimal Mobile Elements.";  
RL BMC Genomics 5:23-23(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MS11;  
RX PubMed=15084227;  
RA Snyder L.A., Davies J.K., Saunders N.J.;  
RT "Microarray genotyping of key experimental strains of Neisseria  
RT gonorrhoeae reveals gene complement diversity and five new neisserial  
RT genes associated with Minimal Mobile Elements.";  
RL BMC Genomics 5:23-23(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=MS11;  
RA Snyder L.A., Davies J.K., Saunders N.J.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY386266; AAS16521.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1227 MW; BACCB286379D1A6 CRC64;  
  
Query Match 42.9%; Score 24; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 LTIW 9  
Db 3 MTFW 7  
  
RESULT 8  
AAS16521  
ID AAS16521 PRELIMINARY; PRT; 10 AA.  
AC AAS16521;

DT 20-MAY-2004 (Tremblrel. 27, Created)  
DT 20-MAY-2004 (Tremblrel. 27, Last sequence update)  
DT 20-MAY-2004 (Tremblrel. 27, Last annotation update)  
DE NuOL (Fragment).  
GN NuOL.  
OS Neisseria gonorrhoeae.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=485;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MS11;  
RX PubMed=15084227;  
RA Snyder L.A., Davies J.K., Saunders N.J.;  
RT "Microarray genotyping of key experimental strains of Neisseria  
RT gonorrhoeae reveals gene complement diversity and five new neisserial  
RT genes associated with Minimal Mobile Elements.";  
RL BMC Genomics 5:23-23(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MS11;  
RA Snyder L.A.S., Davies J.K., Saunders N.J.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY386266; AAS16521.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1227 MW; BACCB286379D1A6 CRC64;  
  
Query Match 42.9%; Score 24; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 LTIW 9  
Db 3 MTFW 7  
  
RESULT 9  
Q85DB0  
ID Q85DB0 PRELIMINARY; PRT; 9 AA.  
AC Q85DB0;  
DT 01-JUN-2003 (Tremblrel. 24, Created)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Lepilemur septentrionalis (northern sportive lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.  
OX NCBI\_TaxID=78584;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy  
RT lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224597; AAP33652.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1 1  
SQ SEQUENCE 9 AA; 1174 MW; 16C563636B5045B0 CRC64;  
  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTW 9  
Db 5 YW---WG 8  
  
RESULT 10

Q85DB8  
ID Q85DB8 PRELIMINARY; PRT; 9 AA.  
AC Q85DB8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Lepilemur edwardsi (Milne-Edwards's sportive lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.  
ON NCBI\_TaxID=122230;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).  
DR EMBL; AF224595; AAP33644.1; --.  
GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db 5 YW---WG 8  
  
RESULT 11  
Q94NA9  
ID Q94NA9 PRELIMINARY; PRT; 9 AA.  
AC Q94NA9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Daubentonia madagascariensis (Aye-aye).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentoniidae;  
OC Daubentonia.  
ON NCBI\_TaxID=31869;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates) based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22281620; PubMed=12393004;  
RA Pastorini J., Forstner M.R., Martin R.D.;  
RT "Phylogenetic relationships among Lemuridae (Primates): evidence from mtDNA.";  
RL J. Hum. Evol. 43:463-478 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).  
DR EMBL; AF224641; AAK70615.1; --.  
DR EMBL; AF224642; AAK70619.1; --.

DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db 5 YW---WG 8  
  
RESULT 12  
Q94NB0  
ID Q94NB0 PRELIMINARY; PRT; 9 AA.  
AC Q94NB0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus rufus (Brown mouse lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
OC Microcebus.  
ON NCBI\_TaxID=122232;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).  
DR EMBL; AF224636; AAK70595.1; --.  
DR EMBL; AF224637; AAK70599.1; --.  
DR EMBL; AF224638; AAK70603.1; --.  
DR EMBL; AF224639; AAK70607.1; --.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db 5 YW---WG 8  
  
RESULT 13  
Q94NB1  
ID Q94NB1 PRELIMINARY; PRT; 9 AA.  
AC Q94NB1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus ravelobensis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
OC Microcebus.  
OX NCBI\_TaxID=122231;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)  
RT based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy  
RT lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224630; AAK70571.1; -.  
DR EMBL; AF224631; AAK70575.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
Qy 3 YWLTWIG 9  
Db 5 YW---WG 8  
  
RESULT 14  
Q94NB2 ID Q94NB2 PRELIMINARY; PRT; 9 AA.  
AC Q94NB2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus murinus (Lesser mouse lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
OC Microcebus.  
OX NCBI\_TaxID=30608;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)  
RT based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy  
RT lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224624; AAK70547.1; -.  
DR EMBL; AF224625; AAK70551.1; -.  
DR EMBL; AF224626; AAK70555.1; -.  
DR EMBL; AF224627; AAK70559.1; -.  
DR EMBL; AF224628; AAK70563.1; -.  
DR EMBL; AF224629; AAK70567.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
Qy 3 YWLTWIG 9  
Db 5 YW---WG 8  
  
RESULT 15  
Q94XE6 ID Q94XE6 PRELIMINARY; PRT; 9 AA.  
AC Q94XE6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit III (Fragment).  
GN Name=cox3;  
OS Tectocoris diophthalmus (cotton harlequin bug).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;  
OC Tectocoris.  
OX NCBI\_TaxID=159956;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396409; PubMed=11504862;  
RA Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;  
RT "Increased rate of gene rearrangement in the mitochondrial genomes of  
RT three orders of hemipteroid insects.";  
RL Mol. Biol. Evol. 18:1828-1832(2001).  
DR EMBL; AF335990; AAK55283.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;  
  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
Qy 3 YWLTWIG 9  
Db 5 YW---WG 8  
  
Search completed: December 29, 2004, 21:41:52  
Job time : 101 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 69.6226 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	96.4	10	5 ABP53931	Abp53931 VEGFR-3 b
2	54	96.4	10	5 ABP53932	Abp53932 VEGFR-3 b
3	43	76.8	13	6 AAO26093	Aao26093 FC region
4	43	76.8	13	8 ADJ50760	Adj50760 Human ser
5	43	76.8	474	6 ABU30004	Abu30004 Protein e
6	43	76.8	492	7 ADC97318	Adc97318 E. faeciu
7	42	75.0	120	4 AAB62747	Aab62747 Human HIV
8	42	75.0	1140	4 AAE09365	Aae09365 Human ATP
9	42	75.0	1498	4 AAE09362	Aae09362 Mouse ATP
10	42	75.0	1503	2 AAY43544	Aay43544 A human M
11	42	75.0	1503	4 AAE09361	Aae09361 Human ATP
12	42	75.0	1503	4 AAE09370	Aae09370 Human ATP
13	42	75.0	1503	4 AAE09367	Aae09367 Human ATP
14	42	75.0	1503	4 AAE09368	Aae09368 Human ATP
15	42	75.0	1503	4 AAE09369	Aae09369 Human ATP
16	42	75.0	1503	4 AAE09364	Aae09364 Human ATP
17	42	75.0	1503	4 AAE09371	Aae09371 Human ATP
18	42	75.0	1503	4 AAE09363	Aae09363 Human ATP
19	42	75.0	1503	5 ABP52113	Abp52113 Homo sapi
20	41	73.2	14	6 AAO26134	Aao26134 FC region
21	41	73.2	14	8 ADJ50801	Adj50801 Human ser
22	41	73.2	34	4 ABB38460	Abb38460 Peptide #
23	41	73.2	34	4 AAM31901	Aam31901 Peptide #
24	41	73.2	34	4 AAM71604	Aam71604 Human bon
25	41	73.2	34	4 AAM59071	Aam59071 Human bra

26	41	73.2	34	4	ABG53286	Abg53286 Human liv
27	41	73.2	34	5	ABG41416	Abg41416 Human pep
28	41	73.2	222	2	AAAY00213	Aay00213 Enterococ
29	41	73.2	222	5	ABP43432	Abp43432 E faecali
30	41	73.2	222	6	ABU88460	Abu88460 E. faecal
31	41	73.2	222	6	ABU13711	Abu13711 Enterococ
32	41	73.2	229	7	ADH85745	Adh85745 Enterococ
33	41	73.2	266	2	AAAY00212	Aay00212 Enterococ
34	41	73.2	266	5	ABP43431	Abp43431 E faecali
35	41	73.2	266	6	ABU88459	Abu88459 E. faecal
36	41	73.2	266	6	ABU13710	Abu13710 Enterococ
37	41	73.2	567	8	ADN46152	Adn46152 Thermococ
38	40	71.4	116	2	AAR15437	Aar15437 Heavy cha
39	40	71.4	116	6	ABO27261	Abo27261 ICAM-1 bi
40	40	71.4	116	6	ABO27269	Abo27269 ICAM-1 bi
41	40	71.4	116	6	ABO27263	Abo27263 ICAM-1 bi
42	40	71.4	116	6	ABO27259	Abo27259 ICAM-1 bi
43	40	71.4	116	6	ABO27255	Abo27255 ICAM-1 bi
44	40	71.4	116	6	ABO27277	Abo27277 Humanised
45	40	71.4	116	6	ABO27273	Abo27273 Murine 1A

ALIGNMENTS

RESULT 1  
ABP53931  
ID ABP53931 standard; peptide; 10 AA.  
XX

AC ABP53931;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:34.  
XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytotatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX Homo sapiens.  
OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "any amino acid"  
FT Misc-difference 10 /note= "any amino acid"  
FT

PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB0000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX

PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;  
PI WPI; 2002-691521/74.  
XX

DR New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
XX diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
PT

XX Claim 12; Page 80; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and

CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 96.4%; Score 54; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.091;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
DB |||||||  
2 GYWLTIWG 9  
  
RESULT 2  
ABP53932  
ID ABP53932 standard; peptide; 10 AA.  
XX  
AC ABP53932;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:35.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnerary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 13; Page 80; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 96.4%; Score 54; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.091;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
DB |||||||  
2 GYWLTIWG 9  
  
RESULT 3  
AAO26093  
ID AAO26093 standard; peptide; 13 AA.  
XX  
AC AAO26093;  
XX  
DT 03-APR-2003 (first entry)  
XX  
DE Fc region binding peptide SEQ ID No 73.  
XX  
KW Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;  
KW antibody response; half-life; stability; circulatory system.  
XX  
OS Unidentified.  
XX  
PN WO200286070-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 18-APR-2002; 2002WO-US012492.  
XX  
PR 18-APR-2001; 2001US-0284534P.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Rondon IJ, Wu Q, Ley AC, Stochl M, Ransohoff TC, Potter MD;  
XX  
DR WPI; 2003-201220/19.  
XX  
PT New polypeptides, useful as binding molecules for detecting, isolating or  
PT purifying immunoglobulin Fc-region polypeptides present in a solution, or  
PT for regulating or preventing an antibody response.  
XX  
PS Claim 3; Page 76; 152pp; English.  
XX  
CC The invention relates to novel isolated polypeptides comprising a  
CC sequence that binds an immunoglobulin Fc region. The polypeptides are  
CC useful as binding molecules for detecting, isolating or purifying  
CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole  
CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are  
CC also useful for regulating or preventing an antibody response, or for  
CC increasing the half-life and over all stability of a therapeutic or  
CC diagnostic compound that is administered to or enters the circulatory  
CC system of an individual. This sequence represents an Fc region binding  
CC peptide of the invention  
XX  
SQ Sequence 13 AA;  
  
Query Match 76.8%; Score 43; DB 6; Length 13;  
Best Local Similarity 62.5%; Pred. No. 5.2;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
DB ||| :||

XX	Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW	Enterococcus faecium.
XX	WO200277183-A2.
OS	03-OCT-2002.
XX	21-MAR-2002; 2002WO-US009107.
PN	21-MAR-2001; 2001US-00815242.
XX	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	(ELIT-) ELITRA PHARM INC.
PA	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI	WPI; 2003-029926/02.
PI	N-PSDB; ACA33874.
DR	New antisense nucleic acids, useful for identifying proteins or screening
DR	for homologous nucleic acids required for cellular proliferation to
XX	isolate candidate molecules for rational drug discovery programs.
PS	Claim 25; SEQ ID NO 57928; 1766pp; English.
XX	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for
CC	proliferation; (7) identifying a compound that influences the activity of
CC	the gene product or that has an activity against a biological pathway
CC	required for proliferation, or that inhibits cellular proliferation; (8)
CC	identifying a gene required for cellular proliferation or the biological
CC	pathway in which a proliferation-required gene or its gene product lies
CC	or a gene on which the test compound that inhibits proliferation of an
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC	compound's activity; (11) a culture comprising strains in which the gene
CC	product is overexpressed or underexpressed; (12) determining the extent
CC	to which each of the strains is present in a culture or collection of
CC	strains; or (13) identifying the target of a compound that inhibits the
CC	proliferation of an organism. The antisense nucleic acids are useful for
CC	identifying proteins or screening for homologous nucleic acids required
CC	for cellular proliferation to isolate candidate molecules for rational
CC	drug discovery programs, or for screening homologous nucleic acids
CC	required for proliferation in cells other than S. aureus, S. typhimurium,
CC	K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC	the target prokaryotic essential genes. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 474 AA;
	Query Match 76.8%; Score 43; DB 6; Length 474;
	Best Local Similarity 85.7%; Pred. No. 1.8e+02;
	Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2 GYWLTIW 8
Db	94 GYWLTCW 100

Db	1 GYWCNVWG 8
RESULT 4	
ADJ50760	
ID	ADJ50760 standard; peptide; 13 AA.
XX	
AC	ADJ50760;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Human serum albumin binding peptide, Seq ID No 297.
XX	
KW	human serum albumin; HSA; serum; blood; tumour; human.
XX	
OS	Homo sapiens.
XX	
PN	WO2003106493-A1.
XX	
PD	24-DEC-2003.
XX	
PF	16-JUN-2003; 2003WO-US018896.
XX	
PR	14-JUN-2002; 2002US-0388642P.
XX	
PA	(DYAX-) DYAX CORP.
XX	
PI	Sato AK, Dawson BM;
XX	
DR	WPI; 2004-082161/08.
XX	
PT	Evaluating sample comprising soluble serum protein by forming complex
PT	comprising serum protein and physically associated compounds using
PT	peptide ligand that specifically binds with proteins, which is separated
PT	and evaluated.
XX	
PS	Disclosure; SEQ ID NO 297; 191pp; English.
XX	
CC	The invention relates to a method of evaluating sample by providing a
CC	soluble serum protein (I), one or more compounds physically associated
CC	with (I), and a (I)-binding agent that comprises a peptide that
CC	specifically binds to (I), allowing the (I)-binding agent to bind to (I)
CC	to form a complex including one or more compounds physically associated
CC	with (I), separating the complex from one or more components of the
CC	sample, and evaluating one or more of the physically associated
CC	compounds. The sample comprises blood or serum, or is obtained from a
CC	biopsy. The sample may also be obtained from a tumour or a region within
CC	5 mm of a tumour. The method is useful for detecting modulators that
CC	modulate interaction of serum protein-binding compound and serum protein
CC	and for identifying binding ligands for serum protein. The present
CC	sequence represents a serum albumin-binding peptide identified using the
CC	method of the invention.
XX	
SQ	Sequence 13 AA;
	Query Match 76.8%; Score 43; DB 8; Length 13;
	Best Local Similarity 62.5%; Pred. No. 5.2;
	Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy	2 GYWLTIWG 9
Db	1 GYWCNVWG 8
RESULT 5	
ABU30004	
ID	ABU30004 standard; protein; 474 AA.
XX	
AC	ABU30004;
XX	
DT	19-JUN-2003 (first entry)
XX	
DE	Protein encoded by Prokaryotic essential gene #15531.

RESULT 6  
ADC97318  
ID ADC97318 standard; protein; 492 AA.  
XX  
AC ADC97318;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE E. faecium protein sequence SEQ ID 6945.  
XX  
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;  
KW abdominal-pelvic infection.  
XX  
OS Enterococcus faecium.  
XX  
PN US6583275-B1.  
XX  
PD 24-JUN-2003.  
XX  
PF 30-JUN-1998; 98US-00107532.  
XX  
PR 02-JUL-1997; 97US-0051571P.  
PR 14-MAY-1998; 98US-0085598P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-799836/75.  
DR N-PSDB; ADC93664.  
XX  
PS New isolated nucleic acid derived from Enterococcus faecium encoding an  
XX Enterococcus faecium polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.  
XX  
PS Example 1; SEQ ID NO 6945; 243pp; English.  
XX  
CC The invention relates to an isolated nucleic acid derived from  
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcripition regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids is useful for diagnosing pathological conditions  
CC resulting from E. faecium bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of Candida albicans -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.  
XX  
SQ Sequence 492 AA;  
  
Query Match 76.8%; Score 43; DB 7; Length 492;  
Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GYWLTIW 8  
Db 112 GYWLTCW 118  
  
RESULT 7  
AAB62747  
ID AAB62747 standard; protein; 120 AA.  
XX

AC AAB62747;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Human HIV-1 monoclonal antibody SEQ ID NO: 46.  
XX  
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KW envelope glycoprotein; gp120; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200100678-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-US017327.  
XX  
PR 30-JUN-1999; 99US-0141701P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Watkins BA, Reitz MS;  
XX  
DR WPI; 2001-112438/12.  
DR N-PSDB; AAF29048.  
XX  
PT Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal.  
XX  
PS Claim 1; Page 51-52; 81pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection  
XX  
SQ Sequence 120 AA;  
  
Query Match 75.0%; Score 42; DB 4; Length 120;  
Best Local Similarity 62.5%; Pred. No. 65;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
Db 104 GYWVSYG 111  
  
RESULT 8  
AAE09365  
ID AAE09365 standard; protein; 1140 AA.  
XX  
AC AAE09365;  
XX  
DT 19-NOV-2001 (first entry)  
XX  
DE Human ATP-binding cassette transporter ABCC6, MRP6 truncated mutant.  
XX  
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;  
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;  
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;  
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200162977-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-US005741.





FT Misc-difference 1274 /note= "encoded by ACT"  
FT Misc-difference 1287 /note= "encoded by TGC"  
FT Misc-difference 1455 /note= "encoded by TTC"  
FT Misc-difference 1455 /note= "encoded by CCC"  
XX WO9949735-A1.  
XX 07-OCT-1999.  
PD 26-MAR-1999; 99WO-US006644.  
XX 27-MAR-1998; 98US-0079759P.  
PR 03-AUG-1998; 98US-0095153P.  
XX (FOXC-) FOX CHASE CANCER CENT.  
XX Kruh G, Lee K, Belinsky M, Bain L;  
PI WPI; 1999-610812/52.  
XX N-PSDB; AA230081.  
DR New transporter gene useful for screening for anti-cancer drugs.  
XX Claim 39; Page 144-147; 153pp; English.  
PS The present sequence represents a human MPR-related ABC transporter  
XX (MOAT) protein, designated MOAT-E. The protein comprises a multi-domain  
CC structure including a tandem repeat of nucleotide binding folds appended  
CC C-terminal to a hydrophobic domain, having Walker A and B ATP binding  
CC sites and several potential membrane spanning domains. The MOAT nucleic  
CC acids are useful for screening a test compound for inhibition of MOAT  
CC mediated transport, indicated by restoration of anticancer drug  
CC sensitivity, which in turn causes a reduction of transporter mediated  
CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as  
CC probes to detect the presence or expression of genes encoding MOAT  
CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating  
XX MOAT proteins  
XX Sequence 1503 AA;  
SQ Query Match 75.0%; Score 42; DB 2; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GYWLTIW 8  
Db 965 GYWLSLW 971  
RESULT 11  
AAE09361  
ID AAE09361 standard; protein; 1503 AA.  
XX AAE09361;  
AC AAE09361;  
XX 19-NOV-2001 (first entry)  
XX Human ATP-binding cassette transporter ABCC6 (MRP6) protein.  
DE Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;  
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;  
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;  
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.  
XX Homo sapiens.  
OS Key Location/Qualifiers  
XX Region 656. .679  
FT /note= "Nucleotide binding fold-1 (NFB-1) region"  
FT 747. .768

FT Region /note= "Nucleotide binding fold-1 (NFB-1) region"  
FT 775. .784  
FT Region /note= "Nucleotide binding fold-1 (NFB-1) region"  
FT 1292. .1307  
FT Region /note= "Nucleotide binding fold-2 (NFB-2) region"  
FT 1321. .1327  
FT Region /note= "Nucleotide binding fold-2 (NFB-2) region"  
FT 1403. .1433  
FT Region /note= "Nucleotide binding fold-2 (NFB-2) region"  
XX WO200162977-A2.  
PN 30-AUG-2001.  
XX 23-FEB-2001; 2001WO-US005741.  
PF 23-FEB-2000; 2000US-0184269P.  
PR (PXEI-) PXE INT INC.  
XX (UYHA-) UNIV HAWAII.  
PA Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;  
PI WPI; 2001-536645/59.  
XX N-PSDB; AAD16230, AAD16231.  
DR Screening presence of Pseudoxanthoma elasticum mutation useful for  
XX identifying homozygotes, compound heterozygotes or carriers involves  
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.  
PS Example 2; Fig 3; 163pp; English.  
XX The invention relates to methods and compositions for diagnosing and  
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological  
CC dysfunctions. The invention is useful for screening for the presence of a  
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding  
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-  
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa  
CC protein located in the plasma membrane containing 17 membrane- spanning  
CC helices grouped into three transmembrane domains. PXE is inherited as an  
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is  
CC a heritable disorder characterised by mineralisation of elastic fibers in  
CC skin, arteries and the retina, that result in dermal lesions with  
CC associated laxity and loss of elasticity, arterial insufficiency,  
CC cardiovascular disease and retinal haemorrhages leading to macular  
CC degeneration. The method is useful for screening a population of  
CC individuals in order to identify individuals with one or more PXE  
CC associated MRP6 alleles who are then provided with appropriate genetic  
CC counselling in view of the PXE status. The methods are useful for  
CC identifying homozygotes, compound heterozygotes or carriers and thus are  
CC useful in the area of genetic testing, carrier detection and prenatal  
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)  
CC transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since  
CC ABCC6 protein is involved in drug-resistance it is also called Multidrug  
CC Resistance associated protein 6 (MRP6)  
XX  
SQ Sequence 1503 AA;  
Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GYWLTIW 8  
Db 965 GYWLSLW 971  
RESULT 12  
AAE09370  
ID AAE09370 standard; protein; 1503 AA.  
XX  
AC AAE09370;  
XX

DT 19-NOV-2001 (first entry)  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) R1314W mutant.  
XX  
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;  
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;  
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;  
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1314  
FT /note= "Wild type Arg substituted with Trp"  
XX  
PN WO200162977-A2.  
XX  
PD 30-AUG-2001.  
PF 23-FEB-2001; 2001WO-US005741.  
XX 23-FEB-2000; 2000US-0184269P.  
XX (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
XX  
PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;  
XX WPI; 2001-536645/59.  
DR N-PSDB; AAD16263.  
XX  
PT Screening presence of Pseudoxanthoma elasticum mutation useful for  
PT identifying homozygotes, compound heterozygotes or carriers involves  
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.  
XX  
PS Claim 13; Page; 163pp; English.  
XX  
CC The invention relates to methods and compositions for diagnosing and  
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological  
CC dysfunctions. The invention is useful for screening for the presence of a  
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding  
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-  
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa  
CC protein located in the plasma membrane containing 17 membrane- spanning  
CC helices grouped into three transmembrane domains. PXE is inherited as an  
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is  
CC a heritable disorder characterised by mineralisation of elastic fibers in  
CC skin, arteries and the retina, that result in dermal lesions with  
CC associated laxity and loss of elasticity, arterial insufficiency,  
CC cardiovascular disease and retinal haemorrhages leading to macular  
CC degeneration. The method is useful for screening a population of  
CC individuals in order to identify individuals with one or more PXE  
CC associated MRP6 alleles who are then provided with appropriate genetic  
CC counselling in view of the PXE status. The methods are useful for  
CC identifying homozygotes, compound heterozygotes or carriers and thus are  
CC useful in the area of genetic testing, carrier detection and prenatal  
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)  
CC transporter, ABCC6 (MRP6) R1314W mutant protein. Note: The present  
CC sequence is not shown in the specification but is derived from human ATP-  
CC binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in  
XX figure 3 of the specification (AAE09361)  
SQ Sequence 1503 AA;  
Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GYWLTIW 8  
Db 965 GYWLSLW 971

RESULT 13  
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ID AAE09367 standard; protein; 1503 AA.  
XX  
AC AAE09367;  
XX  
DT 19-NOV-2001 (first entry)  
XX  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) V1298F mutant.  
XX  
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;  
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;  
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;  
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1298  
FT /note= "Wild type Val substituted with Phe"  
XX  
PN WO200162977-A2.  
XX  
PD 30-AUG-2001.  
PF 23-FEB-2001; 2001WO-US005741.  
XX 23-FEB-2000; 2000US-0184269P.  
XX (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
XX  
PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;  
XX WPI; 2001-536645/59.  
DR N-PSDB; AAD16260.  
XX  
PT Screening presence of Pseudoxanthoma elasticum mutation useful for  
PT identifying homozygotes, compound heterozygotes or carriers involves  
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.  
XX  
PS Claim 13; Page; 163pp; English.  
XX  
CC The invention relates to methods and compositions for diagnosing and  
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological  
CC dysfunctions. The invention is useful for screening for the presence of a  
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding  
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-  
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa  
CC protein located in the plasma membrane containing 17 membrane- spanning  
CC helices grouped into three transmembrane domains. PXE is inherited as an  
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is  
CC a heritable disorder characterised by mineralisation of elastic fibers in  
CC skin, arteries and the retina, that result in dermal lesions with  
CC associated laxity and loss of elasticity, arterial insufficiency,  
CC cardiovascular disease and retinal haemorrhages leading to macular  
CC degeneration. The method is useful for screening a population of  
CC individuals in order to identify individuals with one or more PXE  
CC associated MRP6 alleles who are then provided with appropriate genetic  
CC counselling in view of the PXE status. The methods are useful for  
CC identifying homozygotes, compound heterozygotes or carriers and thus are  
CC useful in the area of genetic testing, carrier detection and prenatal  
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)  
CC transporter, ABCC6 (MRP6) V1298F mutant protein. Note: The present  
CC sequence is not shown in the specification but is derived from human ATP-  
CC binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in  
XX figure 3 of the specification (AAE09361)  
SQ Sequence 1503 AA;



CC	useful in the area of genetic testing, carrier detection and prenatal																										
CC	diagnosis. The present sequence is human ATP-binding cassette (ABC																										
CC	transporter, ABCC6 (MRP6) G1302R mutant protein. Note: The present																										
CC	sequence is not shown in the specification but is derived from human ATP-																										
CC	binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in																										
CC	figure 3 of the specification (AAE09361)																										
XX																											
SQ	Sequence 1503 AA;																										
Query Match 75.0%; Score 42; DB 4; Length 1503;																											
Best Local Similarity 71.4%; Pred. No. 7.7e+02;																											
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;																											
QY	2	GYWLTIW 8																									
		:																									
Db	965	GYWLSLW 971																									
RESULT 15																											
AAE09369																											
ID	AAE09369 standard; protein; 1503 AA.																										
XX																											
AC	AAE09369;																										
XX																											
DT	19-NOV-2001 (first entry)																										
XX																											
DE	Human ATP-binding cassette transporter ABCC6 (MRP6) A1303P mutant.																										
XX																											
KW	Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;																										
KW	Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;																										
KW	ATP-binding cassette transporter; arterial insufficiency; chromosome 16;																										
KW	Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;																										
KW	mutant; mutein.																										
XX																											
OS	Homo sapiens.																										
OS	Synthetic.																										
XX																											
FH	Key	Location/Qualifiers																									
FT	Misc-difference 1302	/note= "Wild type Gly substituted with Arg"																									
FT																											
XX																											
PN	WO200162977-A2.																										
XX																											
PD	30-AUG-2001.																										
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PF	23-FEB-2001; 2001WO-US005741.																										
XX																											
PR	23-FEB-2000; 2000US-0184269P.																										
XX																											
PA	(PXEI-) PXE INT INC.																										
PA	(UYHA-) UNIV HAWAII.																										
XX																											
PI	Boyd CD,	Csiszar K,	Lesaux O,	Urban Z,	Terry S;																						
XX																											
DR	WPI; 2001-536645/59.																										
DR	N-PSDB; AAD16261.																										
XX																											
CC	Screening presence of pseudoxanthoma elasticum mutation useful for																										
PT	identifying homozygotes, compound heterozygotes or carriers involves																										
PT	determining presence of mutation in MRP6 (ABCC6) nucleic acid.																										
XX																											
PS	Claim 13; Page; 163pp; English.																										
XX																											
CC	The invention relates to methods and compositions for diagnosing and																										
CC	treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological																										
CC	dysfunctions. The invention is useful for screening for the presence of a																										
CC	PXE mutation. Mutations associated with PXE maps to the ATP-binding																										
CC	cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-																										
CC	6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa																										
CC	protein located in the plasma membrane containing 17 membrane- spanning																										
CC	helices grouped into three transmembrane domains. PXE is inherited as an																										
CC	autosomal recessive phenotype or appears as a sporadic phenotype. PXE is																										
CC	a heritable disorder characterised by mineralisation of elastic fibers in																										
CC	skin, arteries and the retina, that result in dermal lesions with																										
CC	associated laxity and loss of elasticity, arterial insufficiency,																										
CC	cardiovascular disease and retinal haemorrhages leading to macular																										
CC	degeneration. The method is useful for screening a population of																										
CC	individuals in order to identify individuals with one or more PXE																										
CC	associated MRP6 alleles who are then provided with appropriate genetic																										
CC	counselling in view of the PXE status. The methods are useful for																										
CC	identifying homozygotes, compound heterozygotes or carriers and thus are																										

useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) G1302R mutant protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in figure 3 of the specification (AAE09361)

Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
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Db 965 GYWLSLW 971

RESULT 15  
AAE09369  
ID AAE09369 standard; protein; 1503 AA.  
XX  
AC AAE09369;  
XX  
DT 19-NOV-2001 (first entry)  
XX  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) A1303P mutant.  
XX  
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;  
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;  
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;  
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1303 /note= "Wild type Ala substituted with Pro"  
FT  
XX  
PN WO200162977-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-US005741.  
XX  
PR 23-FEB-2000; 2000US-0184269P.  
XX  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
XX  
PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;  
XX  
DR WPI; 2001-536645/59.  
DR N-PSDB; AAD16262.  
XX  
PT Screening presence of Pseudoxanthoma elasticum mutation useful for  
PT identifying homozygotes, compound heterozygotes or carriers involves  
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.  
XX  
PS Claim 13; Page; 163pp; English.  
XX  
CC The invention relates to methods and compositions for diagnosing and  
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological  
CC dysfunctions. The invention is useful for screening for the presence of a  
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding  
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-  
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa  
CC protein located in the plasma membrane containing 17 membrane- spanning  
CC helices grouped into three transmembrane domains. PXE is inherited as an  
CC a heritable disorder characterised by mineralisation of elastic fibers in  
CC skin, arteries and the retina, that result in dermal lesions with  
CC associated laxity and loss of elasticity, arterial insufficiency,  
CC cardiovascular disease and retinal haemorrhages leading to macular  
CC degeneration. The method is useful for screening a population of  
CC individuals in order to identify individuals with one or more PXE  
CC associated MRP6 alleles who are then provided with appropriate genetic  
CC counselling in view of the PXE status. The methods are useful for  
CC identifying homozygotes, compound heterozygotes or carriers and thus are

CC skin, arteries and the retina, that result in dermal lesions with  
CC associated laxity and loss of elasticity, arterial insufficiency,  
CC cardiovascular disease and retinal haemorrhages leading to macular  
CC degeneration. The method is useful for screening a population of  
CC individuals in order to identify individuals with one or more PXE  
CC associated MRP6 alleles who are then provided with appropriate genetic  
CC counselling in view of the PXE status. The methods are useful for  
CC identifying homozygotes, compound heterozygotes or carriers and thus are  
CC useful in the area of genetic testing, carrier detection and prenatal  
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)  
CC transporter, ABCC6 (MRP6) A1303P mutant protein. Note: The present  
CC sequence is not shown in the specification but is derived from human ATP-  
CC binding cassette transporter ABCC6 (MRP6) protein [SBD ID NO: 3] shown in  
CC figure 3 of the specification (AAE09361)

XX

SQ Sequence 1503 AA;

Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
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Db 965 GYWLTLW 971

Search completed: December 30, 2004, 13:07:50  
Job time : 72.6226 secs



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QM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 23.0189 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTIWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	76.8	492	4 US-09-107-532A-6945	Sequence 6945, Ap
2	42	75.0	1498	4 US-09-792-616-9	Sequence 9, Appli
3	42	75.0	1503	4 US-09-792-616-3	Sequence 3, Appli
4	41	73.2	222	4 US-09-071-035-408	Sequence 408, App
5	41	73.2	229	4 US-09-134-000C-3630	Sequence 3630, Ap
6	41	73.2	266	4 US-09-071-035-406	Sequence 406, App
7	40	71.4	668	4 US-09-248-796A-19350	Sequence 19350, A
8	39	69.6	478	4 US-09-107-532A-6868	Sequence 6868, Ap
9	38	67.9	328	4 US-09-540-236-2629	Sequence 2629, Ap
10	37	66.1	24	4 US-09-270-767-41173	Sequence 41173, A
11	37	66.1	24	4 US-09-270-767-56389	Sequence 56389, A
12	37	66.1	132	4 US-09-248-796A-22785	Sequence 22785, A
13	37	66.1	278	4 US-09-145-828A-11	Sequence 11, Appl
14	37	66.1	278	4 US-09-903-456-18	Sequence 18, Appl
15	37	66.1	499	4 US-09-252-991A-23328	Sequence 23328, A
16	37	66.1	591	4 US-09-561-077C-18	Sequence 18, Appl
17	37	66.1	591	4 US-09-221-014-18	Sequence 18, Appl
18	37	66.1	865	4 US-09-252-991A-19339	Sequence 19339, A
19	36.5	65.2	612	4 US-09-252-991A-19134	Sequence 19134, A
20	36	64.3	119	2 US-08-318-157B-5	Sequence 5, Appli
21	36	64.3	119	4 US-09-253-794-5	Sequence 5, Appli
22	36	64.3	172	4 US-09-107-532A-6560	Sequence 6560, Ap
23	36	64.3	219	3 US-09-247-373B-52	Sequence 52, Appl
24	36	64.3	242	2 US-08-512-955-4	Sequence 4, Appli
25	36	64.3	247	4 US-09-252-991A-26736	Sequence 26736, A
26	36	64.3	268	2 US-08-861-512-3	Sequence 3, Appli
27	36	64.3	280	1 US-08-414-685-2	Sequence 2, Appli

28	36	64.3	367	4 US-09-248-796A-15188	Sequence 15188, A
29	36	64.3	1528	1 US-08-463-092B-6	Sequence 6, Appli
30	36	64.3	1528	2 US-08-462-109A-6	Sequence 6, Appli
31	36	64.3	1528	2 US-08-460-907B-6	Sequence 6, Appli
32	36	64.3	1528	3 US-08-463-179A-6	Sequence 6, Appli
33	36	64.3	1528	3 US-08-461-384B-6	Sequence 6, Appli
34	36	64.3	1531	1 US-08-141-893-2	Sequence 2, Appli
35	36	64.3	1531	1 US-08-463-092B-2	Sequence 2, Appli
36	36	64.3	1531	1 US-08-463-092B-4	Sequence 4, Appli
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42	36	64.3	1531	3 US-08-463-179A-4	Sequence 4, Appli
43	36	64.3	1531	3 US-08-461-384B-2	Sequence 2, Appli
44	36	64.3	1531	3 US-08-461-384B-4	Sequence 4, Appli
45	36	64.3	1531	3 US-08-407-207A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-107-532A-6945  
; Sequence 6945, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6945:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 492 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...492  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6945:  
US-09-107-532A-6945

Query Match 76.8%; Score 43; DB 4; Length 492;  
Best Local Similarity 85.7%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | | |  
Db 112 GYWLTCW 118

RESULT 2  
US-09-792-616-9  
; Sequence 9, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-792-616-9

Query Match 75.0%; Score 42; DB 4; Length 1498;  
Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | | |  
Db 960 GYWLTLW 966

RESULT 3  
US-09-792-616-3  
; Sequence 3, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 1503  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-792-616-3

Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
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Db 965 GYWLTLW 971

RESULT 4  
US-09-071-035-408  
; Sequence 408, Application US/09071035  
; Patent No. 6448043  
; GENERAL INFORMATION:

; APPLICANT: Gil H. Choi  
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 496  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,035  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brooks  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB369P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 408:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 222 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-071-035-408

Query Match 73.2%; Score 41; DB 4; Length 222;  
Best Local Similarity 62.5%; Pred. No. 59;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9  
| | | | |  
Db 179 GTWITLW 186

RESULT 5  
US-09-134-000C-3630  
; Sequence 3630, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3630  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-3630

Query Match 73.2%; Score 41; DB 4; Length 229;  
Best Local Similarity 62.5%; Pred. No. 61;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9



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RESULT 9
US-09-540-236-2629
; Sequence 2629, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2629
; LENGTH: 328
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2629

Query Match          67.9%; Score 38; DB 4; Length 328;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      | |||:|
Db      116 GQWLTW 122

RESULT 10
US-09-270-767-41173
; Sequence 41173, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41173
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-41173

Query Match          66.1%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 YWLTIWG 9
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Db      16 HWLSLWG 22

RESULT 11
US-09-270-767-56389
; Sequence 56389, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56389
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56389
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Query Match          66.1%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 YWLTIWG 9
      :||:|
Db      16 HWLSLWG 22

RESULT 12
US-09-248-796A-22785
; Sequence 22785, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22785
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (6),(77),(85)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-22785

Query Match          66.1%; Score 37; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTI 7
      |||||
Db      123 GYWLTI 128

RESULT 13
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match          66.1%; Score 37; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
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Job time : 24.0189 secs

Db 108 GYWIFLW 114  
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RESULT 14  
US-09-903-456-18  
; Sequence 18, Application US/09903456  
; Patent No. 6677145  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda Eun-Yeong  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Pereira, Suzette L.  
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF  
; FILE REFERENCE: 6407.US.P3  
; CURRENT APPLICATION NUMBER: US/09/903,456  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: US 09/624,670  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: US 09/379,095  
; PRIOR FILING DATE: 1999-08-23  
; PRIOR APPLICATION NUMBER: US 09/145,828  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-903-456-18

Query Match 66.1%; Score 37; DB 4; Length 278;  
Best Local Similarity 57.1%; Pred. No. 2.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
|||: :|  
Db 108 GYWIFLW 114

RESULT 15  
US-09-252-991A-23328  
; Sequence 23328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23328  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23328

Query Match 66.1%; Score 37; DB 4; Length 499;  
Best Local Similarity 57.1%; Pred. No. 5e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
|||: :|  
Db 111 GYWISAW 117

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
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(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTIMGX 10  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1599051 seqs, 35972711 residues  
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Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep:\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	96.4	10	13 US-10-046-922-34	Sequence 34, Appl
2	54	96.4	10	13 US-10-046-922-35	Sequence 35, Appl
3	43	76.8	13	14 US-10-125-869A-73	Sequence 73, Appl
4	43	76.8	13	15 US-10-462-262-297	Sequence 297, App
5	43	76.8	474	15 US-10-282-122A-57928	Sequence 57928, A
6	43	76.8	671	16 US-10-437-963-190740	Sequence 190740,
7	42	75.0	1498	10 US-09-792-616-9	Sequence 9, Appli
8	42	75.0	1498	16 US-10-764-328-9	Sequence 9, Appli
9	42	75.0	1503	10 US-09-792-616-3	Sequence 3, Appli
10	42	75.0	1503	16 US-10-764-328-3	Sequence 3, Appli
11	41	73.2	14	14 US-10-125-869A-114	Sequence 114, App
12	41	73.2	14	15 US-10-462-262-338	Sequence 338, App
13	41	73.2	34	9 US-09-864-761-43458	Sequence 43458, A

14	41	73.2	82	15	US-10-424-599-240891	Sequence 240891,
15	41	73.2	222	9	US-09-071-035-408	Sequence 408, App
16	41	73.2	222	14	US-10-206-576-408	Sequence 408, App
17	41	73.2	266	9	US-09-071-035-406	Sequence 406, App
18	41	73.2	266	14	US-10-206-576-406	Sequence 406, App
19	40	71.4	101	15	US-10-424-599-194869	Sequence 194869,
20	40	71.4	116	10	US-09-910-483-1	Sequence 1, Appli
21	40	71.4	116	10	US-09-910-483-5	Sequence 5, Appli
22	40	71.4	116	10	US-09-910-483-9	Sequence 9, Appli
23	40	71.4	116	10	US-09-910-483-13	Sequence 13, Appl
24	40	71.4	116	10	US-09-910-483-17	Sequence 17, Appl
25	40	71.4	116	10	US-09-910-483-21	Sequence 21, Appl
26	40	71.4	116	10	US-09-910-483-25	Sequence 25, Appl
27	40	71.4	116	10	US-09-910-483-29	Sequence 29, Appl
28	40	71.4	116	10	US-09-910-483-33	Sequence 33, Appl
29	40	71.4	116	10	US-09-910-483-37	Sequence 37, Appl
30	40	71.4	116	10	US-09-910-483-41	Sequence 41, Appl
31	40	71.4	116	10	US-09-910-483-43	Sequence 43, Appl
32	40	71.4	138	14	US-10-160-232-86	Sequence 86, Appl
33	40	71.4	138	14	US-10-160-232-90	Sequence 90, Appl
34	40	71.4	373	14	US-10-369-493-8834	Sequence 8834, Ap
35	39	69.6	13	14	US-10-125-869A-75	Sequence 75, Appl
36	39	69.6	13	15	US-10-462-262-299	Sequence 299, App
37	39	69.6	57	15	US-10-424-599-226815	Sequence 226815,
38	39	69.6	86	17	US-10-425-115-188067	Sequence 188067,
39	39	69.6	91	14	US-10-156-761-13764	Sequence 13764, A
40	39	69.6	162	9	US-09-738-626-5178	Sequence 5178, Ap
41	39	69.6	452	14	US-10-091-007-88	Sequence 88, Appl
42	39	69.6	474	15	US-10-282-122A-52805	Sequence 52805, A
43	39	69.6	475	15	US-10-282-122A-57680	Sequence 57680, A
44	39	69.6	794	9	US-09-738-626-4579	Sequence 4579, Ap
45	38.5	68.8	101	17	US-10-425-115-260407	Sequence 260407,

ALIGNMENTS

RESULT 1  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 96.4%; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIMG 9

Db 2 GYWLTIMG 9

RESULT 2  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
US-10-046-922-35

Query Match 96.4%; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
Db 2 GYWLTIWG 9  
RESULT 3  
US-10-125-869A-73  
; Sequence 73, Application US/10125869A  
; Publication No. US20030199671A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac Jesus  
; APPLICANT: Wu, Qi-Long  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Stochl, Mark  
; APPLICANT: Ransohoff, Thomas C.  
; APPLICANT: Potter, M. Daniel (deceased)  
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION  
; TITLE OF INVENTION: POLYPEPTIDES  
; FILE REFERENCE: 3421.1006-001  
; CURRENT APPLICATION NUMBER: US/10/125,869A  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/284,534  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc region binding polypeptide  
US-10-125-869A-73

Query Match 76.8%; Score 43; DB 14; Length 13;  
Best Local Similarity 62.5%; Pred. No. 10;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
Db 1 GYWCNVWG 8  
RESULT 4  
US-10-462-262-297  
; Sequence 297, Application US/10462262  
; Publication No. US20040009534A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Dawson, Bruce M.

; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: 10280-052001  
; CURRENT APPLICATION NUMBER: US/10/462,262  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/388,642  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 430  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 297  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin binding polypeptide  
US-10-462-262-297

Query Match 76.8%; Score 43; DB 15; Length 13;  
Best Local Similarity 62.5%; Pred. No. 10;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
Db 1 GYWCNVWG 8

RESULT 5  
US-10-282-122A-57928  
; Sequence 57928, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57928  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Enterococcus faecium

US-10-282-122A-57928

Query Match 76.8%; Score 43; DB 15; Length 474;  
Best Local Similarity 85.7%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||||  
Db 94 GYWLTCW 100

RESULT 6

US-10-437-963-190740  
; Sequence 190740, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 190740  
; LENGTH: 671  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87125C.1.pep  
US-10-437-963-190740

Query Match 76.8%; Score 43; DB 16; Length 671;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YWLTIWG 9  
|||  
Db 329 YWTTIWG 335

RESULT 7

US-09-792-616-9  
; Sequence 9, Application US/09792616  
; Publication No. US20030165828A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-792-616-9

Query Match 75.0%; Score 42; DB 10; Length 1498;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||||

Db 960 GYWLSLW 966

RESULT 8

US-10-764-328-9  
; Sequence 9, Application US/10764328  
; Publication No. US20040166521A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001PC  
; CURRENT APPLICATION NUMBER: US/10/764,328  
; CURRENT FILING DATE: 2004-01-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-764-328-9

Query Match 75.0%; Score 42; DB 16; Length 1498;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||||  
Db 960 GYWLSLW 966

RESULT 9

US-09-792-616-3  
; Sequence 3, Application US/09792616  
; Publication No. US20030165828A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 1503  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-792-616-3

Query Match 75.0%; Score 42; DB 10; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||||  
Db 965 GYWLSLW 971

RESULT 10

US-10-764-328-3  
; Sequence 3, Application US/10764328  
; Publication No. US20040166521A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001PC  
; CURRENT APPLICATION NUMBER: US/10/764,328  
; CURRENT FILING DATE: 2004-01-23



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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-328-3

Query Match      75.0%; Score 42; DB 16; Length 1503;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
Db      965 GYWLSLW 971

RESULT 11
US-10-125-869A-114
; Sequence 114, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-114

Query Match      73.2%; Score 41; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIW 9
Db      1 GFWCTFWG 8

RESULT 12
US-10-462-262-338
; Sequence 338, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-338

Query Match      73.2%; Score 41; DB 15; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIW 9
Db      1 GFWCTFWG 8

RESULT 13
US-09-864-761-43458
; Sequence 43458, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43458
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000403.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4  
US-09-864-761-43458

Query Match 73.2%; Score 41; DB 9; Length 34;  
Best Local Similarity 62.5%; Pred. No. 46;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | | | | : : |  
Db 25 GYMITVFG 32

RESULT 14  
US-10-424-599-240891  
; Sequence 240891, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 240891  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(82)  
; OTHER INFORMATION: unsure at all Xaa locations  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_59551C.1.pep  
US-10-424-599-240891

Query Match 73.2%; Score 41; DB 15; Length 82;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | | | : |  
Db 76 GYWLNLW 82

RESULT 15  
US-09-071-035-408  
; Sequence 408, Application US/09071035  
; Publication No. US20020045737A1  
; GENERAL INFORMATION:  
; APPLICANT: Gil H. Choi  
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 496  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,035

; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brookes  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB369P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 408:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 222 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-071-035-408

Query Match 73.2%; Score 41; DB 9; Length 222;  
Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | | | | : : |  
Db 179 GTWITLWG 186

Search completed: December 30, 2004, 13:50:00  
Job time : 75.5283 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	75.0	441	2 C95307	probable transport
2	42	75.0	1502	2 T42216	multidrug resistan
3	41	73.2	391	2 PC4117	replication protei
4	41	73.2	419	2 E90446	permease imported
5	40	71.4	142	2 C34903	Ig heavy chain pre
6	40	71.4	425	2 B71038	probable Na+/H+-ex
7	40	71.4	508	2 C95282	probable ABC trans
8	39	69.6	376	2 AF1978	hypothetical prote
9	39	69.6	475	2 T46745	arginine/ornithine
10	39	69.6	490	2 C86879	arginine/ornithine
11	38	67.9	118	2 T35739	probable integral
12	38	67.9	426	2 C75176	na+/h+ antiporter
13	38	67.9	477	2 G90251	ABCtransporter [im
14	38	67.9	583	2 T50103	probable oxidoredu
15	38	67.9	829	2 S58888	Ins P4-binding pro
16	38	67.9	829	2 S71847	Ins P4-binding pro
17	37.5	67.0	1063	2 A33830	cation efflux syst
18	37.5	67.0	1063	2 JC4700	cadmium, zinc, cob
19	37	66.1	123	1 AVMS14	Ig heavy chain v r
20	37	66.1	167	2 AF0881	probable exported
21	37	66.1	172	2 AI2232	hypothetical prote
22	37	66.1	187	1 S13868	ubiquinol-cytochro
23	37	66.1	197	2 AF2356	hypothetical prote
24	37	66.1	218	2 S76385	hypothetical prote
25	37	66.1	286	2 E88690	protein F4H10.7 [
26	37	66.1	292	2 S49164	LysR-type protein
27	37	66.1	360	2 S74751	CDP-glucose 4,6-de
28	37	66.1	380	2 S12839	Ig heavy chain pre
29	37	66.1	416	2 AF1127	rod shape-determin

30	37	66.1	472	2 E83497	probable amino aci
31	37	66.1	482	2 JH0110	arginine/ornithine
32	37	66.1	497	2 G86878	arginine/ornithine
33	36.5	65.2	607	2 F82966	probable transcarb
34	36	64.3	164	2 F69990	hypothetical prote
35	36	64.3	171	2 E83140	phosphatidylglycer
36	36	64.3	239	2 H85756	partial probable m
37	36	64.3	241	2 G82391	hypothetical prote
38	36	64.3	247	2 G81013	1-acyl-sn-glycerol
39	36	64.3	247	2 A81957	1-acylglycerol-3-p
40	36	64.3	250	2 A69843	hypothetical prote
41	36	64.3	280	2 S61111	GPI2 protein - yea
42	36	64.3	292	2 A83779	hypothetical prote
43	36	64.3	351	2 D84541	hypothetical prote
44	36	64.3	385	2 S43540	YSD83 protein - ye
45	36	64.3	387	2 B90862	probable membrane

ALIGNMENTS

RESULT 1

C95307

probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) mag  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: C95307

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse  
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti;  
A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: C95307

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-441 <KUR>

A;Cross-references: UNIPROT:Q922T6; GB:AE006469; PIDN:AAK65021.1; PID:gl4523451; GSPDB:G

A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaullt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Sma0684

A;Genome: plasmid

C;Superfamily: L-lysine transport protein

Query Match 75.0%; Score 42; DB 2; Length 441;  
Best Local Similarity 71.4%; Pred. No. 32;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8

Db 92 GYWISIW 98

RESULT 2

T42216

multidrug resistance-associated protein homolog MLP-1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T42216

R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.

Mol. Pharmacol. 53, 1068-1075, 1998

A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mair  
A;Reference number: Z22081; MUID:98279126; PMID:9614210

A;Accession: T42216

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
A;Residues: 1-1502 <HIR>  
A;Cross-references: UNIPROT:O88269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3242457  
A;Experimental source: strain Sprague-Dawley; liver  
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 75.0%; Score 42; DB 2; Length 1502;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
||||:|  
Db 964 GYWLSLW 970

RESULT 3  
PC4117  
replication protein homolog - Pyrococcus sp. (fragment)  
N;Alternate names: hypothetical 391 protein  
C;Species: Pyrococcus sp.  
C;Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 17-May-1996  
C;Accession: PC4117  
R;Rashid, N.; Morikawa, M.; Imanaka, T.  
Gene 166, 139-143, 1995  
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.  
A;Reference number: JC4514; MUID:96105215; PMID:8529878  
A;Accession: PC4117  
A;Molecule type: DNA  
A;Residues: 1-391 <RAS>  
A;Cross-references: DDBJ:D50018

Query Match 73.2%; Score 41; DB 2; Length 391;  
Best Local Similarity 85.7%; Pred. No. 41;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YWLTIWG 9  
||||||  
Db 155 YWLTWEG 161

RESULT 4  
E90446  
permease [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: E90446  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: E90446  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-419 <KUR>  
A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G  
C;Genetics:  
A;Gene: SSO2718

Query Match 73.2%; Score 41; DB 2; Length 419;  
Best Local Similarity 62.5%; Pred. No. 43;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
|:| |:  
Db 365 GFWETLWG 372

RESULT 5  
C34903  
Ig heavy chain precursor V region (5-27) - mouse  
C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
C;Accession: C34903  
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A;Title: Active site structure and antigen binding properties of idiotypically cross-react  
A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: C34903  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-142 <BED>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 40; DB 2; Length 142;  
Best Local Similarity 62.5%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
||| ||  
Db 126 GYWFAYWG 133

RESULT 6  
B71038  
probable Na+/H+-exchanging protein - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C;Accession: B71038  
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: B71038  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-425 <KAW>  
A;Cross-references: UNIPROT:O59255; GB:AP000006; NID:g3236133; PIDN:BAA30706.1; PID:g3258  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH1594

Query Match 71.4%; Score 40; DB 2; Length 425;  
Best Local Similarity 75.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | | | |  
Db 319 GAWLTAWG 326

RESULT 7  
C95282  
probable ABC transporter, periplasmic solute-binding protein, family 5 Sma0302 [imported]  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: C95282  
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot:  
A;Reference number: A95262; MUID:21396509; PMID:11481432  
A;Accession: C95282  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-508 <KUR>  
A;Cross-references: UNIPROT:Q930N2; GB:AE006469; PIDN:AAK64821.1; PID:g14523232; GSPDB:G  
A;Experimental source: strain 1021, megaplasmid pSymA  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.



Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: SMA0302  
A;Genome: plasmid

Query Match 71.4%; Score 40; DB 2; Length 508;  
Best Local Similarity 85.7%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
||| |||  
Db 393 GYWDTIW 399

RESULT 8  
AF1978  
hypothetical protein alr1377 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AF1978  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AF1978  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-376 <KUR>  
A;Cross-references: UNIPROT:Q8YX40; GB:BA000019; PIDN:BA000019; PID:gl7130724; GSPDB:G  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr1377

Query Match 69.6%; Score 39; DB 2; Length 376;  
Best Local Similarity 75.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIW 9  
| | | | |  
Db 124 GEWLRIWG 131

RESULT 9  
T46745  
arginine/ornithine antiporter [imported] - Lactobacillus sakei  
C;Species: Lactobacillus sakei  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T46745  
R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez,  
J. Bacteriol. 180, 4154-4159, 1998  
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of  
A;Reference number: Z23141; MUID:98361904; PMID:9696763  
A;Accession: T46745  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-475 <ZUN>  
A;Cross-references: UNIPROT:O53092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:g2  
C;Genetics:  
A;Gene: arcD  
C;Function:  
A;Description: necessary for arginine transport; involved in ornithine-arginine exchange  
A;Pathway: arginine catabolism  
C;Superfamily: L-lysine transport protein

Query Match 69.6%; Score 39; DB 2; Length 475;  
Best Local Similarity 71.4%; Pred. No. 99;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
||| |  
Db 94 GYWLSAW 100

RESULT 10  
C86879  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL1403  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: C86879  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: C86879  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-490 <STO>  
A;Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:gl2725084; PIDN:AAK06133.1; GSPDB:GB  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: arcD1  
C;Superfamily: L-lysine transport protein

Query Match 69.6%; Score 39; DB 2; Length 490;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
||| |  
Db 93 GYWLSAW 99

RESULT 11  
T35739  
probable integral membrane protein - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C;Accession: T35739  
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.  
submitted to the EMBL Data Library, August 1999  
A;Reference number: Z21588  
A;Accession: T35739  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-118 <SAU>  
A;Cross-references: UNIPROT:Q9S2K9; EMBL:AL109732; PIDN:CAB52050.1; GSPDB:GN00070; SCOEDI  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCODDB:SC7H2.08  
C;Superfamily: Streptomyces coelicolor probable integral membrane protein SC7H2.08

Query Match 67.9%; Score 38; DB 2; Length 118;  
Best Local Similarity 57.1%; Pred. No. 38;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YWLTIWG 9  
: | | : | |  
Db 51 FWLSLWG 57

RESULT 12  
C75176  
na+/h+ antiporter (napa-2) PAB0390 - Pyrococcus abyssi (strain Orsay)  
C;Species: Pyrococcus abyssi  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: C75176  
R;anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc

A;Reference number: A75001 A;Accession: C75176 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-426 <KAW> A;Cross-references: UNIPROT:Q9V160; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4949 A;Experimental source: strain Orsay C;Genetics: A;Gene: napA-2; PAB0390 C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1		Db		244 GRWPTIWG 251	
Query Match 67.9%; Score 38; DB 2; Length 426; Best Local Similarity 62.5%; Pred. No. 1.3e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		QY		2 GYWLTIWG 9	
Db		320 GAWITAWG 327			
RESULT 13 G90251 ABCTransporter [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: G90251 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan- Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome. A;Reference number: A99139 A;Accession: G90251 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-477 <KUR> A;Cross-references: UNIPROT:Q97ZC3; GB:AE006641; NID:g13814184; PIDN:AAK41270.1; GSPDB:Q C;Genetics: A;Gene: SSO0999		Query Match 67.9%; Score 38; DB 2; Length 829; Best Local Similarity 62.5%; Pred. No. 2.4e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		QY	
		Db		689 GHWLCCWG 696	
RESULT 14 T50103 probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004 C;Accession: T50103 R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, January 2000 A;Reference number: Z25038 A;Accession: T50103 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-583 <SEE> A;Cross-references: UNIPROT:Q9US28; EMBL:AL136499; PIDN:CAB66164.1; GSPDB:GN00066; SPDB: A;Experimental source: strain 972h(-); cosmid c1783 C;Genetics: A;Gene: SPDB:SPAC1783.01 A;Map position: 1		Query Match 67.9%; Score 38; DB 2; Length 477; Best Local Similarity 66.7%; Pred. No. 1.4e+02; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		QY	
		Db		415 WITVWG 420	
RESULT 14 T50103 probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004 C;Accession: T50103 R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, January 2000 A;Reference number: Z25038 A;Accession: T50103 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-583 <SEE> A;Cross-references: UNIPROT:Q9US28; EMBL:AL136499; PIDN:CAB66164.1; GSPDB:GN00066; SPDB: A;Experimental source: strain 972h(-); cosmid c1783 C;Genetics: A;Gene: SPDB:SPAC1783.01 A;Map position: 1		Query Match 67.9%; Score 38; DB 2; Length 583; Best Local Similarity 75.0%; Pred. No. 1.7e+02; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		QY	
		Db		2 GYWLTIWG 9	

Db 244 GRWPTIWG 251

RESULT 15  
S58888  
Ins P4-binding protein - human  
C;Species: Homo sapiens (man)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 04-Apr-2004  
C;Accession: S58888  
R;Cullen, P.J.; Hsuan, J.J.; Truong, O.; Letcher, A.J.; Jackson, T.R.; Dawson, A.P.; Irv-  
Nature 376, 527-530, 1995  
A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the  
A;Reference number: S58888; MUID:95364929; PMID:7637787  
A;Accession: S58888  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-829 <CUL>  
A;Cross-references: EMBL:X89399  
F;328-539/Domain: ras-specific GAP catalytic domain homology <GAP>  
F;571-670/Domain: pleckstrin repeat homology <PLK>

Query Match 67.9%; Score 38; DB 2; Length 829;  
Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
Db 689 GHWLCCWG 696

Search completed: December 30, 2004, 13:17:12  
Job time : 13.6761 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWVG 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	76.8	221	2 Q74JK6	Q74jk6 lactobacill
2	43	76.8	221	2 AAS08923	Aas08923 lactobaci
3	43	76.8	733	2 Q8H2N7	Q8h2n7 oryza sativ
4	42	75.0	284	2 Q6MC01	Q6mc01 parachlamyd
5	42	75.0	284	2 CAF23898	Caf23898 parachlam
6	42	75.0	441	2 Q92ZT6	Q92zt6 rhizobium m
7	42	75.0	1308	2 Q8T6H2	Q8t6h2 dictyosteli
8	42	75.0	1498	1 MRP6_MOUSE	Q9rlb7 mus musculu
9	42	75.0	1502	1 MRP6_RAT	O88269 rattus norv
10	42	75.0	1503	1 MRP6_HUMAN	O95255 homo sapien
11	41	73.2	266	2 Q82Z85	O82z85 enterococcu
12	41	73.2	376	2 Q6CBE4	Q6cbe4 yarrowia li
13	41	73.2	413	2 Q9HKA9	Q9hka9 thermoplas
14	41	73.2	419	2 Q97VB7	Q97vb7 sulfolobus
15	41	73.2	736	2 Q8DMV4	Q8dmv4 synchococc
16	41	73.2	1052	2 Q7YZ84	Q7yz84 plasmodium
17	41	73.2	1652	2 Q74DR3	Q74dr3 geobacter s
18	41	73.2	1652	2 AAR34628	Aar34628 geobacter
19	40	71.4	167	1 OB_MACMU	Q28504 macaca mula
20	40	71.4	331	2 Q775C7	Q775c7 bordetella
21	40	71.4	331	2 AAR97683	Aar97683 bordetell
22	40	71.4	401	2 Q9KHQ6	Q9khq6 bacteroides
23	40	71.4	425	2 O59255	O59255 pyrococcus
24	40	71.4	508	2 Q930N2	Q930n2 rhizobium m
25	40	71.4	1970	2 Q88H71	Q88h71 pseudomonas
26	39	69.6	91	2 Q82A22	Q82a22 streptomyce
27	39	69.6	117	2 Q7S013	Q7s013 neurospora
28	39	69.6	144	2 Q6M566	Q6m566 corynebacte
29	39	69.6	144	2 CAF21531	Caf21531 corynebac
30	39	69.6	162	2 Q8NQB6	Q8nqb6 corynebacte
31	39	69.6	253	2 O32816	O32816 lactococcus

32	39	69.6	257	2 Q9ARZ0	Q9arz0 oryza sativ
33	39	69.6	312	2 Q6C129	Q6c129 yarrowia li
34	39	69.6	376	2 Q8YX40	Q8yx40 anabaena sp
35	39	69.6	432	2 Q8ZUS8	Q8zus8 pyrobaculum
36	39	69.6	443	2 Q7NSJ2	Q7nsj2 chromobacte
37	39	69.6	459	2 Q9KGV3	Q9kgv3 lactococcus
38	39	69.6	469	2 Q6TK71	Q6tk71 streptococc
39	39	69.6	469	2 AAR30325	Aar30325 streptoco
40	39	69.6	471	2 Q6HP27	Q6hp27 bacillus th
41	39	69.6	471	2 Q73E85	Q73e85 bacillus ce
42	39	69.6	471	2 Q81IH9	Q81ih9 bacillus ce
43	39	69.6	471	2 AAS39409	Aas39409 bacillus
44	39	69.6	475	1 ARCD_LACSK	O53092 lactobacill
45	39	69.6	475	2 Q8DWF9	Q8dwp9 streptococc

ALIGNMENTS

RESULT 1					
Q74JK6					
ID	Q74JK6	PRELIMINARY;	PRT;	221 AA.	
AC	Q74JK6;				
DT	05-JUL-2004 (TrEMBLrel. 27, Created)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)				
DE	Hemolysin-like protein.				
GN	OrderedLocusNames=LJ1101;				
OS	Lactobacillus johnsonii.				
OC	Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;				
OC	Lactobacillus.				
OX	NCBI_TaxID=33959;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NCC 533;				
RX	PubMed=14966310;				
RA	Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,				
RA	Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,				
RA	Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;				
RT	"The genome sequence of the probiotic intestinal bacterium				
RT	Lactobacillus johnsonii NCC 533."				
RL	Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).				
DR	EMBL; AB017203; AAS08923.1; -.				
DR	InterPro; IPR004254; HlyIII_related.				
DR	InterPro; IPR005744; HlyIII.				
DR	Pfam; PF03006; HlyIII; 1.				
DR	TIGRPFAMs; TIGR01065; hlyIII; 1.				
KW	Complete proteome.				
SQ	SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;				
Query Match 76.8%; Score 43; DB 2; Length 221;					
Best Local Similarity 62.5%; Pred. No. 70;					
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;					
QY	2 GYWLTWVG 9				
	: : :				
Db	172 GFWLLVWG 179				
RESULT 2					
AAS08923					
ID	AAS08923	PRELIMINARY;	PRT;	221 AA.	
AC	AAS08923;				
DT	02-MAR-2004 (TrEMBLrel. 27, Created)				
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)				
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)				
DE	Hemolysin-like protein.				
GN	LJ1101.				
OS	Lactobacillus johnsonii.				
OC	Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;				
OC	Lactobacillus.				
OX	NCBI_TaxID=33959;				
RN	[1]				

RP SEQUENCE FROM N.A.  
RC STRAIN=NCC 533;  
RX PubMed=14966310;  
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,  
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,  
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;  
RT "The genome sequence of the probiotic intestinal bacterium  
RL Lactobacillus johnsonii NCC 533.";  
RT Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).  
DR EMBL; AE017203; AAS08923.1; --  
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;  
  
Query Match 76.8%; Score 43; DB 2; Length 221;  
Best Local Similarity 62.5%; Pred. No. 70;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
Db 172 GFWLLVWG 179  
|:|:|:|  
|:|:|:|  
  
RESULT 3  
Q8H2N7 PRELIMINARY; PRT; 733 AA.  
ID Q8H2N7  
AC Q8H2N7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein OJ1138\_B05.118.  
GN Name=OJ1138\_B05.118;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AP005486; BAC16197.1; --  
DR Gramene; Q8H2N7; --  
DR InterPro; IPR007658; DUF594.  
DR Pfam; PF04578; DUF594; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;  
  
Query Match 76.8%; Score 43; DB 2; Length 733;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 YWLTIWG 9  
Db 328 YWTTIWG 334  
|||:|  
|||:|  
  
RESULT 4  
Q6MC01 PRELIMINARY; PRT; 284 AA.  
ID Q6MC01  
AC Q6MC01;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=pc1174;  
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).  
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.  
OX NCBI\_TaxID=264201;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=null;  
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
RA Rattei T., Mewes H.-W., Wagner M.;

RT "Genome sequence of an amoeba symbiont and its use for reconstructing  
RT the evolutionary history of chlamydiae.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BX908798; CAF23898.1; --  
KW Hypothetical protein.  
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;  
  
Query Match 75.0%; Score 42; DB 2; Length 284;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 YWLTIWG 9  
Db 273 YWLSLWG 279  
|||:|  
|||:|  
  
RESULT 5  
CAF23898 PRELIMINARY; PRT; 284 AA.  
ID CAF23898  
AC CAF23898;  
DT 14-APR-2004 (TrEMBLrel. 27, Created)  
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN PC1174.  
OS Parachlamydia sp. UWE25.  
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.  
OX NCBI\_TaxID=264201;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UWE25;  
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
RA Rattei T., Mewes H., Wagner M.;  
RT "Genome sequence of an amoeba symbiont and its use for reconstructing  
RT the evolutionary history of chlamydiae.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UWE25;  
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
RA Rattei T., Mewes H., Wagner M.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BX908798; CAF23898.1; --  
KW Hypothetical protein.  
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;  
  
Query Match 75.0%; Score 42; DB 2; Length 284;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 YWLTIWG 9  
Db 273 YWLSLWG 279  
|||:|  
|||:|  
  
RESULT 6  
Q92ZT6 PRELIMINARY; PRT; 441 AA.  
ID Q92ZT6  
AC Q92ZT6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Probable transport protein.  
GN OrderedLocusNames=RA0363; ORFNames=SMA0684;  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OG Plasmid pSymA.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.



RC STRAIN=1021;  
RX MEDLINE=21396509; PubMed=11481432;  
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,  
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,  
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,  
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;  
RT "Nucleotide sequence and predicted functions of the entire  
RT Sinorhizobium meliloti pSymA megaplasmid.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21368234; PubMed=11474104;  
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,  
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,  
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,  
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,  
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,  
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,  
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,  
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,  
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,  
RA Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;  
RT "The composite genome of the legume symbiont Sinorhizobium meliloti.";  
RL Science 293:668-672(2001).  
DR EMBL; AE007228; AAK65021.1; -.  
DR PIR; C95307; C95307.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Complete proteome; Plasmid; Transmembrane; Transport.  
SQ SEQUENCE 441 AA; 46277 MW; B6F5C9EC96011AD0 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 441;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
Db 92 GYWISIW 98  
|||||

RESULT 7  
Q8T6H2 PRELIMINARY; PRT; 1308 AA.  
AC Q8T6H2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ABC transporter ABCC.7.  
GN Name=abcC7;  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ax4;  
RA Anjard C., Loomis W.F.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY; Belongs to the ABC transporter family.  
DR EMBL; AF474339; AAL85710.1; -.  
DR HSSP; P08716; 1MT0.  
DR DictyBase; DDB0201630; abcC7.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.  
DR GO; GO:0000166; F:nucleotide binding; IEA.  
DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR011527; ABC\_membrane\_1.  
DR InterPro; IPR001140; ABC\_TM\_transpt.  
DR InterPro; IPR003439; ABC\_transporter.  
DR Pfam; PF00664; ABC\_membrane; 2.  
DR Pfam; PF00005; ABC\_tran; 2.  
DR SMART; SM00382; AAA; 2.  
DR PROSITE; PS50929; ABC\_TM1F; 2.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 2.  
KW ATP-binding.  
SQ SEQUENCE 1308 AA; 149576 MW; 336120ACBF737AC1 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 1308;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YWLTIW 8  
Db 764 YWLTIW 769  
|||||

RESULT 8  
MRP6\_MOUSE STANDARD; PRT; 1498 AA.  
ID MRP6\_MOUSE  
AC Q9R1S7; Q80YB6;  
DT 01-OCT-2004 (Rel. 45, Created)  
DT 01-OCT-2004 (Rel. 45, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6).  
GN Name=Abcc6; Synonyms=Mrp6;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ddy; TISSUE=Liver;  
RA Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;  
RT "Mus musculus mRNA for multidrug resistance-associated protein 6 (MRP6), complete cds.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 685-1498 FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Liver;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP REVIEW.  
RX DOI=10.1038/mp.a002623.01;  
RA Beck C., Le Saux O., Varadi A., Boyd C.;  
RT "Abcc6.";  
RL (er) AfCS-Nature Molecule Pages (2004).



```
CC -!- FUNCTION: May participate directly in the active transport of
CC drugs into subcellular organelles or influence drug distribution
CC indirectly (By similarity).
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CC
CC -----
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CC -----
CC EMBL; AB028737; BAA83820.1; -.
CC EMBL; BC049980; AAH49980.1; -.
CC HSSP; Q03518; 1JJ7.
CC MGD; MGI:1351634; Abcc6.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001140; ABC_TM_transpt.
CC InterPro; IPR003439; ABC_transporter.
CC InterPro; IPR005292; MRP_assoc.
CC Pfam; PF00664; ABC_membrane; 2.
CC Pfam; PF00005; ABC_tran; 2.
CC ProDom; PD000006; ABC_transporter; 1.
CC SMART; SM00382; AAA; 2.
CC TIGRFAMs; TIGR00957; MRP_assoc_pro; 1.
CC PROSITE; PS0929; ABC_TM1F; 2.
CC PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
CC PROSITE; PS0893; ABC_TRANSPORTER_2; 2.
CC ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.
KW DOMAIN 1 37 Extracellular (By similarity).
FT TRANSMEM 38 58 1 (By similarity).
FT DOMAIN 59 78 Cytoplasmic (By similarity).
FT TRANSMEM 79 99 2 (By similarity).
FT DOMAIN 100 104 Extracellular (By similarity).
FT TRANSMEM 105 125 3 (By similarity).
FT DOMAIN 126 137 Cytoplasmic (By similarity).
FT TRANSMEM 138 155 4 (By similarity).
FT DOMAIN 156 173 Extracellular (By similarity).
FT TRANSMEM 174 194 5 (By similarity).
FT DOMAIN 195 300 Cytoplasmic (By similarity).
FT TRANSMEM 301 321 6 (By similarity).
FT DOMAIN 322 347 Extracellular (By similarity).
FT TRANSMEM 348 368 7 (By similarity).
FT DOMAIN 369 424 Cytoplasmic (By similarity).
FT TRANSMEM 425 445 8 (By similarity).
FT DOMAIN 446 448 Extracellular (By similarity).
FT TRANSMEM 449 469 9 (By similarity).
FT DOMAIN 470 531 Cytoplasmic (By similarity).
FT TRANSMEM 532 552 10 (By similarity).
FT DOMAIN 553 574 Extracellular (By similarity).
FT TRANSMEM 575 595 11 (By similarity).
FT DOMAIN 596 934 Cytoplasmic (By similarity).
FT TRANSMEM 935 955 12 (By similarity).
FT DOMAIN 956 992 Extracellular (By similarity).
FT TRANSMEM 993 1013 13 (By similarity).
FT DOMAIN 1014 1056 Cytoplasmic (By similarity).
FT TRANSMEM 1057 1077 14 (By similarity).
FT DOMAIN 1078 1078 Extracellular (By similarity).
FT TRANSMEM 1079 1099 15 (By similarity).
FT DOMAIN 1100 1170 Cytoplasmic (By similarity).
FT TRANSMEM 1171 1191 16 (By similarity).
FT DOMAIN 1192 1193 Extracellular (By similarity).
FT TRANSMEM 1194 1214 17 (By similarity).
FT DOMAIN 1215 1498 Cytoplasmic (By similarity).
FT DOMAIN 627 851 ABC_transporter 1.
FT DOMAIN 1260 1494 ABC_transporter 2.
FT NP_BIND 661 ATP (Potential).
FT NP_BIND 1294 1301 ATP (Potential).
FT CARBOHYD 21 21 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 341 341 N-linked (GlcNAc. .) (Potential).
FT CONFLICT 706 706 A -> V (in Ref. 2).
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FT CONFLICT 927 927 I -> T (in Ref. 2).
FT CONFLICT 1401 1401 H -> Q (in Ref. 2).
FT CONFLICT 1448 1448 L -> V (in Ref. 2).
FT CONFLICT 1477 1477 N -> S (in Ref. 2).
SQ SEQUENCE 1498 AA; 164788 MW; EFCFF33FOEEC813C CRC64;

Query Match 75.0%; Score 42; DB 1; Length 1498;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
Db 960 GYWLSLW 966

RESULT 9
MRP6 RAT STANDARD; PRT; 1502 AA.
ID_MRP6 RAT
AC O88269;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-
DE family C, member 6) (MRP-like protein-1) (MLP-1).
GN Name=Abcc6; Synonyms=Mrp6, Mlp1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=98279126; PubMed=9614210;
RA Hirohashi T., Suzuki H., Ito K., Ogawa K., Kume K., Shimizu T.,
RA Sugiyama Y.;
RT "Hepatic expression of multidrug resistance-associated protein-like
RT proteins maintained in eisa hyperbilirubinemic rats.";
RL Mol. Pharmacol. 53:1068-1075(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=20159081; PubMed=10692506;
RA Madon J., Hagenbuch B., Landmann L., Meier P.J., Stieger B.;
RT "Transport function and hepatocellular localization of mrp6 in rat
RT liver.";
RL Mol. Pharmacol. 57:634-641(2000).
CC -!- FUNCTION: May participate directly in the active transport of
CC drugs into subcellular organelles or influence drug distribution
CC indirectly (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: High in liver and lower in duodenum and
CC kidney.
CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CC
CC -----
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CC -----
CC EMBL; AB010466; BAA28954.1; -.
CC EMBL; U73038; AAD12747.1; -.
CC PIR; T42216; T42216.
CC HSSP; P08716; 1MT0.
CC RGD; 620268; Abcc6.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001140; ABC_TM_transpt.
CC InterPro; IPR003439; ABC_transporter.
CC InterPro; IPR005292; MRP_assoc.
CC Pfam; PF00664; ABC_membrane; 2.
CC Pfam; PF00005; ABC_tran; 2.
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DR ProDom; PD000006; ABC\_transporter; 1.  
DR SMART; SMO0382; AAA; 2.  
DR TIGRFAMS; TIGR00957; MRP\_assoc\_pro; 1.  
DR PROSITE; PS0929; ABC\_TMIF; 2.  
DR PROSITE; PS0211; ABC\_TRANSPORTER\_1; 2.  
DR PROSITE; PS0893; ABC\_TRANSPORTER\_2; 2.  
KW ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.  
FT DOMAIN 5 37 Extracellular (By similarity).  
FT TRANSMEM 38 58 1 (By similarity).  
FT DOMAIN 59 78 Cytoplasmic (By similarity).  
FT TRANSMEM 79 99 2 (By similarity).  
FT DOMAIN 100 104 Extracellular (By similarity).  
FT TRANSMEM 105 125 3 (By similarity).  
FT DOMAIN 126 137 Cytoplasmic (By similarity).  
FT TRANSMEM 138 155 4 (By similarity).  
FT DOMAIN 156 173 Extracellular (By similarity).  
FT TRANSMEM 174 194 5 (By similarity).  
FT DOMAIN 195 300 Cytoplasmic (By similarity).  
FT TRANSMEM 301 321 6 (By similarity).  
FT DOMAIN 322 347 Extracellular (By similarity).  
FT TRANSMEM 348 368 7 (By similarity).  
FT DOMAIN 369 424 Cytoplasmic (By similarity).  
FT TRANSMEM 425 445 8 (By similarity).  
FT DOMAIN 446 448 Extracellular (By similarity).  
FT TRANSMEM 449 469 9 (By similarity).  
FT DOMAIN 470 531 Cytoplasmic (By similarity).  
FT TRANSMEM 532 552 10 (By similarity).  
FT DOMAIN 553 574 Extracellular (By similarity).  
FT TRANSMEM 575 595 11 (By similarity).  
FT DOMAIN 596 938 Cytoplasmic (By similarity).  
FT TRANSMEM 939 959 12 (By similarity).  
FT DOMAIN 960 996 Extracellular (By similarity).  
FT TRANSMEM 997 1017 13 (By similarity).  
FT DOMAIN 1018 1060 Cytoplasmic (By similarity).  
FT TRANSMEM 1061 1081 14 (By similarity).  
FT DOMAIN 1082 1082 Extracellular (By similarity).  
FT TRANSMEM 1083 1103 15 (By similarity).  
FT DOMAIN 1104 1174 Cytoplasmic (By similarity).  
FT TRANSMEM 1175 1195 16 (By similarity).  
FT DOMAIN 1196 1197 Extracellular (By similarity).  
FT TRANSMEM 1198 1218 17 (By similarity).  
FT DOMAIN 1219 1502 Cytoplasmic (By similarity).  
FT TRANSMEM 1227 851 ABC transporter 1.  
FT DOMAIN 1264 1498 ABC transporter 2.  
FT NP\_BIND 661 668 ATP (Potential).  
FT NP\_BIND 1298 1305 ATP (Potential).  
FT CARBOHYD 21 21 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 1502 AA; 164995 MW; 539901B674A74A28 CRC64;

Query Match 75.0%; Score 42; DB 1; Length 1502;  
Best Local Similarity 71.4%; Pred. No. 6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
|||:|  
Db 964 GYWLSLW 970

RESULT 10  
MRP6\_HUMAN  
ID MRP6\_HUMAN STANDARD; PRT; 1503 AA.  
AC O95255; P78420; Q9UMZ7;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6) (Anthracycline resistance-associated protein)  
DE (Multi-specific organic anion transporter-E) (MOAT-E).  
DE Name=ABCC6; Synonyms=MRP6, ARA;  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=99107222; PubMed=9892204;  
RX Kool M., van der Linden M., de Haas M., Baas F., Borst P.;  
RA "Expression of human MRP6, a homologue of the multidrug resistance protein gene MRP1, in tissues and cancer cells.";  
RT Cancer Res. 59:175-182(1999).  
RL [2]  
RN [2] SEQUENCE FROM N.A.  
RP MEDLINE=99425270; PubMed=10493829;  
RX Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;  
RA "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";  
RT Genomics 60:295-308(1999).  
RL [3]  
RN [3] SEQUENCE FROM N.A.  
RP MEDLINE=99352020; PubMed=10424734;  
RX Belinsky M.G., Kruh G.D.;  
RA "MOAT-E (ARA) is a full-length MRP/cMOAT subfamily transporter expressed in kidney and liver.";  
RT Br. J. Cancer 80:1342-1349(1999).  
RL [4]  
RN [4] FUNCTION, AND CHARACTERIZATION OF VARIANTS PXE PHE-1298; ARG-1302 AND SER-1321.  
RP MEDLINE=21988190; PubMed=11880368; DOI=10.1074/jbc.M110918200;  
RX Ilias A., Urban Z., Seidl T.L., Le Saux O., Sinko E., Boyd C.D., Sarkadi B., Varadi A.;  
RA "Loss of ATP-dependent transport activity in pseudoxanthoma elasticum-associated mutants of human ABCC6 (MRP6).";  
RT J. Biol. Chem. 277:16860-16867(2002).  
RL [5]  
RN [5] REVIEW, AND VARIANT PXE PRO-455.  
RP MEDLINE=21321623; PubMed=11427982; DOI=10.1016/S1471-4914(00)01869-4;  
RX Uitto J., Pulkkinen L., Ringpfeil F.;  
RA "Molecular genetics of pseudoxanthoma elasticum: a metabolic disorder at the environment-genome interface?";  
RT Trends Mol. Med. 7:13-17(2001).  
RL [6]  
RN [6] VARIANT GLN-1268.  
RP MEDLINE=20374463; PubMed=10913334; DOI=10.1006/bbrc.2000.3101;  
RX Germain D.P., Perdu J., Remones V., Jeunenaitre X.;  
RA "Homozygosity for the R1268Q mutation in MRP6, the pseudoxanthoma elasticum gene, is not disease-causing.";  
RT Biochem. Biophys. Res. Commun. 274:297-301(2000).  
RL [7]  
RN [7] VARIANT ARG-64.  
RP MEDLINE=20514578; PubMed=11058917;  
RX DOI=10.1002/1098-1004(200011)16:5<449::AID-HUMU24>3.0.CO;2-O;  
RA Germain D.P., Perdu J., Remones V., Manzoni K., Jeunenaitre X.;  
RT "Identification of two polymorphisms (c189G>C; c190T>C) in exon 2 of the human MRP6 gene (ABCC6) by screening of Pseudoxanthoma elasticum patients: possible sequence correction?";  
RT Hum. Mutat. 16:449-449(2000).  
RL [8]  
RN [8] VARIANT PXE CYS-1339, AND VARIANT GLN-632.  
RP MEDLINE=20408303; PubMed=10954200;  
RX Struk B., Cai L., Zaech S., Ji W., Chung J., Lumsden A., Stumm M., Huber M., Schaen L., Kim C.-A., Goldsmith L.A., Viljoen D., Figuera L.E., Fuchs W., Munier F., Ramesar R., Hohl D., Richards R., Neldner K.H., Lindpaintner K.;  
RA "Mutations of the gene encoding the transmembrane transporter protein ABC-C6 cause pseudoxanthoma elasticum.";  
RT J. Mol. Med. 78:282-286(2000).  
RL [9]  
RN [9] VARIANTS PXE PRO-1114; GLN-1138 AND TRP-1314, AND VARIANT ALA-614.  
RP MEDLINE=20296630; PubMed=10835642; DOI=10.1038/76102;  
RX Le Saux O., Urban Z., Tschuch C., Csizsar K., Bacchelli B., Quaglini D., Pasquali-Ronchetti I., Pope F.M., Richards A., Terry S., Bercovich L., de Paepe A., Boyd C.D.;  
RA "Mutations in a gene encoding an ABC transporter cause pseudoxanthoma

RT elasticum.";

RL Nat. Genet. 25:223-227(2000).

RN [10]

RP VARIANTS PXE TRP-1138, AND VARIANT GLN-1268.

RX MEDLINE=20283940; PubMed=10811882; DOI=10.1073/pnas.100041297;

RA Ringpfeil F., Lewohl M.G., Christiano A.M., Uitto J.;

RT "Pseudoxanthoma elasticum: mutations in the MRP6 gene encoding a

transmembrane ATP-binding cassette (ABC) transporter.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000).

RN [11]

RP VARIANTS PXE LYS-411; GLN-518; SER-568; PRO-673; GLN-765; PRO-1114;

RP TRP-1121; PRO-1138; GLN-1138; ASP-1203; PHE-1298; ILE-1301; ARG-1302;

RP PRO-1303; GLN-1314; TRP-1314; SER-1321; CYS-1339; HIS-1347; ASN-1361

RP AND THR-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-319;

RP LYS-497; ALA-614; GLN-632; HIS-953; CYS-1241 AND GLN-1268.

RX MEDLINE=21426347; PubMed=11536079;

RA Le Saux O., Beck K., Sachsinger C., Silvestri C., Treiber C.,

RA Goering H.H.H., Johnson E.W., De Paep A., Pope F.M.,

RA Pasquali-Ronchetti I., Bercovitch L., Terry S., Boyd C.D.;

RT "A spectrum of ABCC6 mutations is responsible for pseudoxanthoma

RT elasticum.";

RL Am. J. Hum. Genet. 69:749-764(2001).

RN [12]

RP VARIANTS PXE 60-ARG--TYR-62 DEL; ARG-364 AND ARG-1354, AND VARIANT

RP GLY-265.

RX MEDLINE=21558431; PubMed=11702217; DOI=10.1007/s004390100582;

RA Pulkkinen L., Nakano A., Ringpfeil F., Uitto J.;

RT "Identification of ABC6 pseudogenes on human chromosome 16p:

RT implications for mutation detection in pseudoxanthoma elasticum.";

RL Hum. Genet. 109:356-365(2001).

RN [13]

RP VARIANTS ALA-614; GLN-632 AND GLN-1268.

RX MEDLINE=21632106; PubMed=11776382;

RA Wang J., Near S., Young K., Connelly P.W., Hegele R.A.;

RT "ABCC6 gene polymorphism associated with variation in plasma

RT lipoproteins.";

RL J. Hum. Genet. 46:699-705(2001).

CC -!- FUNCTION: May participate directly in the active transport of

CC drugs into subcellular organelles or influence drug distribution

CC indirectly. Transports glutathione conjugates as Leukotriene-c4

CC (LTC4) and N-ethylmaleimide S-glutathione (NEM-GS).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed in kidney and liver. Very low

CC expression in other tissues.

CC -!- DISEASE: Defects in ABCC6 are a cause of autosomal dominant

CC pseudoxanthoma elasticum (AD-PXE) [MIM:177850]. PXE is a disorder

CC characterized by calcification of elastic fibers in skin, arteries

CC and retina that results in dermal lesions with associated laxity

CC and loss of elasticity, arterial insufficiency and retinal

CC hemorrhages leading to macular degeneration.

CC -!- DISEASE: Defects in ABCC6 are a cause of autosomal recessive

CC pseudoxanthoma elasticum (AR-PXE) [MIM:264800].

CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.

CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous

CC gene model prediction.

CC -!- DATABASE: NAME=Mutations of the ABCC6 gene;

CC NOTE=Retina International's Scientific Newsletter;

CC WWW="http://www.retina-international.com/sci-news/abcc6mut.htm".

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DR EMBL; AF076622; AAC79696.1; --

DR EMBL; U91318; AAC15785.1; ALT\_SEQ.

DR EMBL; AF168791; AAD51293.1; --

DR HSSP; P08716; 1MT0.

DR Genew; HGNC:57; ABCC6.

DR MIM; 603234; --

DR MIM; 177850; --

DR MIM; 264800; --

DR GO; GO:0005624; C:membrane fraction; TAS.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0005524; F:ATP binding; TAS.

DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; TAS.

DR GO; GO:0005215; F:transporter activity; TAS.

DR GO; GO:0042493; P:response to drug; TAS.

DR GO; GO:0006810; P:transport; TAS.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR001140; ABC\_TM\_transpt.

DR InterPro; IPR003439; ABC\_transporter.

DR InterPro; IPR005292; MRP\_assoc.

DR Pfam; PF00664; ABC\_membrane; 2.

DR Pfam; PF00005; ABC\_tran; 2.

DR ProDom; PD000006; ABC\_transporter; 1.

DR SMART; SM00382; AAA; 2.

DR TIGRFAMS; TIGR00957; MRP\_assoc\_pro; 1.

DR PROSITE; PS50929; ABC\_TMIF; 2.

DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 2.

DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 2.

KW ATP-binding; Disease mutation; Glycoprotein; Polymorphism; Repeat;

KW Transmembrane; Transport; Vision.

FT DOMAIN 1 31 Extracellular (By similarity).

FT TRANSMEM 32 52 1 (By similarity).

FT DOMAIN 53 72 Cytoplasmic (By similarity).

FT TRANSMEM 73 93 2 (By similarity).

FT DOMAIN 94 98 Extracellular (By similarity).

FT TRANSMEM 99 119 3 (By similarity).

FT DOMAIN 120 131 Cytoplasmic (By similarity).

FT TRANSMEM 132 149 4 (By similarity).

FT DOMAIN 150 167 Extracellular (By similarity).

FT TRANSMEM 168 188 5 (By similarity).

FT DOMAIN 189 302 Cytoplasmic (By similarity).

FT TRANSMEM 303 323 6 (By similarity).

FT DOMAIN 324 349 Extracellular (By similarity).

FT TRANSMEM 350 370 7 (By similarity).

FT DOMAIN 371 426 Cytoplasmic (By similarity).

FT TRANSMEM 427 447 8 (By similarity).

FT DOMAIN 448 450 Extracellular (By similarity).

FT TRANSMEM 451 471 9 (By similarity).

Query Match 75.0%; Score 42; DB 1; Length 1503;

Best Local Similarity 71.4%; Pred. No. 6e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8

Db 965 GYWLSLW 971

RESULT 11

Q82Z85 PRELIMINARY; PRT; 266 AA.

AC Q82Z85;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN OrderedLocusNames=EF3185;

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI\_TaxID=1351;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=V583 / ATCC 700802;

RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;

RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,

RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,

Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,

Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,

RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,



RA Fraser C.M.;  
RT "Role of mobile DNA in the evolution of vancomycin-resistant  
RL Enterococcus faecalis";  
RL Science 299:2071-2074(2003).  
DR EMBL; AE016957; AA082859.1; -.  
DR TIGR; EF3185; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 266 AA; 28291 MW; CD6E72C4DF555A36 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 266;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
|:|:|  
Db 203 GTWITLWG 210

RESULT 12  
Q6CBE4 PRELIMINARY; PRT; 376 AA.  
AC Q6CBE4;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to sp|P38071 Saccharomyces cerevisiae YBR026c.  
GN ORFNames=YALI0C19624g;  
OS Yarrowia lipolytica (Candida lipolytica).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Dipodascaceae; Yarrowia.  
OX NCBI\_TaxID=4952;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RG GENOLEVURES;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckrich J.M., Beyne E., Bleykasten C.,  
RA Boistrame A., Boyer J., Cattolico L., Confalonieri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts";  
RL Nature 430:35-44(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RA Genoscope;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR382129; CAG82338.1; -.  
SQ SEQUENCE 376 AA; 41206 MW; E085FF7C32379DCB CRC64;

Query Match 73.2%; Score 41; DB 2; Length 376;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||||  
Db 301 GYWLTRW 307

RESULT 13  
Q9HKA9 PRELIMINARY; PRT; 413 AA.  
AC Q9HKA9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update).  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Transport protein related protein.  
GN OrderedLocusNames=ra0692;  
OS Thermoplasma acidophilum.  
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
OC Thermoplasmataceae; Thermoplasma.  
OX NCBI\_TaxID=2303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 1728;  
RX MEDLINE=20479972; PubMed=11029001;  
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;  
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma  
RT acidophilum.";  
RL Nature 407:508-513(2000).  
DR EMBL; AL445065; CAC11830.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR007114; MFS.  
DR PROSITE; PS50850; MFS; 1.  
KW Complete proteome.  
SQ SEQUENCE 413 AA; 45192 MW; 307093BC358063D4 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 413;  
Best Local Similarity 62.5%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
|:|:|  
Db 354 GFWETLWG 361

RESULT 14  
Q97VB7 PRELIMINARY; PRT; 419 AA.  
AC Q97VB7;  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Permease.  
GN OrderedLocusNames=SSO2718;  
OS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,  
RA De Moers A., Erauso G., Fletcher C., Gordon P.M.K.,  
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;  
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
DR EMBL; AE006865; AAK42828.1; -.  
DR PIR; E90446; E90446.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR007114; MFS.  
DR InterPro; IPR005828; Sub transporter.  
DR Pfam; PF00083; Sugar tr; 1.  
DR PROSITE; PS50850; MFS; 1.  
KW Complete proteome.  
SQ SEQUENCE 419 AA; 46499 MW; 6DB6AB6B5C6DA267 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 419;  
Best Local Similarity 62.5%; Pred. No. 2.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
|:| |:|  
Db 365 GFWETLWG 372

RESULT 15

Q8DMV4 Q8DMV4 PRELIMINARY; PRT; 736 AA.

AC Q8DMV4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cellulose synthase.  
GN OrderedLocusNames=tl10007;  
OS Synechococcus elongatus (Thermosynechococcus elongatus).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=32046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BP-1;  
RX MEDLINE=22225144; PubMed=12240834;  
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,  
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the thermophilic cyanobacterium  
RT Thermosynechococcus elongatus BP-1.";  
RL DNA Res. 9:123-130(2002).  
DR EMBL; AP005369; BAC07560.1; -.  
DR InterPro; IPR001173; Glyco\_trans\_2.  
DR Pfam; PF00535; Glycos\_transf\_2; 1.  
KW Complete proteome.  
SQ SEQUENCE 736 AA; 85049 MW; D31C506166FD9624 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 736;  
Best Local Similarity 85.7%; Pred. No. 4.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|:| |:|  
Db 557 GYWLHIW 563



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OM protein - protein search, using sw model  
Run on: December 29, 2004, 21:19:46 ; Search time 94 Seconds  
(without alignments)  
38.163 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2002273 seqs, 358729299 residues  
Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A Geneseq\_23Sep04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	5	ABP53932 VEGFR-3 b
2	54	75.0	10	5	ABP53931 VEGFR-3 b
3	50	69.4	10	5	ABP53968 VEGFR-3 b
4	39.5	54.9	9	5	ABJ04472 Stem cell
5	35.5	49.3	9	5	ABJ04461 Stem cell
6	35	48.6	9	5	ABJ04460 Stem cell
7	33.5	46.5	7	5	ABJ04531 Molt-4 le
8	33	45.8	7	5	ABP53964 VEGFR-3 b
9	33	45.8	8	2	AAJ03715 Fluorine-
10	33	45.8	8	3	AAJ76817 Immunogen
11	33	45.8	8	5	ABP53965 VEGFR-3 b
12	33	45.8	8	7	ADG94005 Immunogen
13	33	45.8	8	8	ADL98014 Peptide h
14	33	45.8	10	5	ABB46346 Desmoglei
15	33	45.8	10	5	ABB46607 Desmocoll
16	32	44.4	7	3	AAJ76794 Somatosta
17	32	44.4	7	5	ABP53418 Backbone
18	32	44.4	9	4	ABP22609 HIV A11 m
19	32	44.4	9	4	ABP20314 HIV A03 m
20	32	44.4	9	5	AAU90543 Insulin/i
21	32	44.4	9	5	AAU90464 Insulin/i
22	32	44.4	9	5	AAU90542 Insulin/i
23	32	44.4	9	5	AAU90541 Insulin/i
24	32	44.4	10	2	AAW43886 Specific
25	32	44.4	10	3	AAJ66209 HLA-A3-bi

26	32	44.4	10	3	AAJ66213	Aay66213 HLA-A11-b
27	32	44.4	10	4	ABP20316	Abp20316 HIV A03 m
28	32	44.4	10	4	ABP20318	Abp20318 HIV A03 m
29	32	44.4	10	4	ABP22613	Abp22613 HIV A11 m
30	32	44.4	10	4	ABP14381	Abp14381 HIV A03 s
31	32	44.4	10	4	ABP22611	Abp22611 HIV A11 m
32	32	44.4	10	5	AAU88395	Aau88395 Insulin/i
33	32	44.4	10	5	AAU90462	Aau90462 Insulin/i
34	32	44.4	10	5	AAU90463	Aau90463 Insulin/i
35	32	44.4	10	5	AAU90535	Aau90535 Insulin/i
36	32	44.4	10	8	ADE64384	Ade64384 Radiophar
37	32	44.4	10	8	ADH58622	Adh58622 Radiophar
38	31	43.1	8	2	AAW97529	Aaw97529 Antigenic
39	31	43.1	9	5	ABP53933	Abp53933 VEGFR-3 b
40	31	43.1	9	5	ABJ04488	Abj04488 HUVEC cel
41	31	43.1	9	8	ADN64476	Adn64476 HLA bindi
42	31	43.1	10	4	AAG95260	Aag95260 Human com
43	30.5	42.4	10	2	AAR14709	Aar14709 Labaditin
44	30	41.7	8	2	AAW12859	Aaw12859 RGP-bind
45	30	41.7	8	3	AAJ91924	Aay91924 Residues

ALIGNMENTS

RESULT 1  
ABP53932  
ID ABP53932 standard; peptide; 10 AA.  
XX  
AC ABP53932;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:35.

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytotatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.

XX Homo sapiens.  
OS Synthetic.

PN WO200257299-A2.

XX 25-JUL-2002.

XX 16-JAN-2002; 2002WO-IB000099.

PR 17-JAN-2001; 2001US-0262476P.

XX (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;

XX WPI; 2002-691521/74.

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
such as cancer and diseases of neovascularization.

PS Claim 13; Page 80; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
antidiabetic and vulnerary activities, and can be used in gene therapy.  
Compositions and methods from the present invention are useful for  
diagnosing, evaluating and treating disorders mediated by the activity of  
the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 100.0%; Score 72; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGYWLTIWGC 10  
Db 1 CGYWLTIWGC 10  
  
RESULT 2  
ABP53931  
ID ABP53931 standard; peptide; 10 AA.  
XX  
AC ABP53931;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:34.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "any amino acid"  
FT Misc-difference 10 /note= "any amino acid"  
FT  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB0000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 12; Page 80; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 75.0%; Score 54; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
Db 2 GYWLTIWG 9  
  
RESULT 3  
ABP53968  
ID ABP53968 standard; peptide; 10 AA.  
XX  
AC ABP53968;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:73.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 5. .7 /note= "X is any amino acid"  
FT Misc-difference 9 /note= "X is any amino acid"  
FT  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB0000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Disclosure; Page 147; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a VEGFR-3 binding peptide, which is given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 69.4%; Score 50; DB 5; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 CGYWLTIWGC 10  
Db ||||| |  
1 CGYWXXXWXC 10  
  
RESULT 4  
ABJ04472  
ID ABJ04472 standard; peptide; 9 AA.  
XX  
AC ABJ04472;  
XX 24-OCT-2002 (first entry)  
XX Stem cell (mesenchymal) targeting peptide 61.  
DE  
XX  
KW BRASIL; targeting peptide; bacterial infection;  
KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;  
KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
KW viral infection; cardiovascular disease; degenerative disease.  
XX  
OS Unidentified.  
XX WO200220822-A2.  
PN 14-MAR-2002.  
PD 07-SEP-2001; 2001WO-US028124.  
PF 08-SEP-2000; 2000US-0231266P.  
XX 17-JAN-2001; 2001US-00765101.  
PR (TEXA ) UNIV TEXAS SYSTEM.  
PA Arap W, Pasqualini R;  
XX WPI; 2002-404697/43.  
DR  
XX  
PT Identification of targeting peptides that can be used to treat diseases  
PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis  
PT of Selective Ligands) method comprises a single differential  
PT centrifugation step.  
XX  
PS Example 5; Page 76; 167pp; English.  
XX  
CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis  
CC of Selective Interactive Ligands) to obtain a targeting peptide. The  
CC BRASIL method of the invention involves: exposing a target to a phage  
CC display library in a first phase; exposing the first phase to a second  
CC phase; and separating the phage bound to the target from unbound phage.  
CC The BRASIL method of the invention allows cell phages to be separated  
CC from the remaining unbound phage in a single differential centrifugation  
CC step. When compared to conventional cell panning methods, the BRASIL  
CC method shows a significant increase in recovery of specific phage and a  
CC substantial decrease in background. The BRASIL method is useful for  
CC identifying targeting peptides. The targeting peptides identified by the  
CC method of the invention are useful for treating disease states, such as:  
CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune  
CC disease; bacterial infection; viral infection; cardiovascular disease and  
CC degenerative disease. The present amino acid sequence represents a

CC targeting peptide of the invention  
XX  
SQ Sequence 9 AA;  
  
Query Match 54.9%; Score 39.5; DB 5; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
  
QY 1 CGYWLTIWGC 10  
Db ||| : |||  
1 CG-WFSWGC 9  
  
RESULT 5  
ABJ04461  
ID ABJ04461 standard; peptide; 9 AA.  
XX  
AC ABJ04461;  
XX 24-OCT-2002 (first entry)  
DT Stem cell (mesenchymal) targeting peptide 50.  
DE  
XX BRASIL; targeting peptide; bacterial infection;  
KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;  
KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
KW viral infection; cardiovascular disease; degenerative disease.  
XX  
OS Unidentified.  
XX WO200220822-A2.  
PN 14-MAR-2002.  
PD 07-SEP-2001; 2001WO-US028124.  
PF 08-SEP-2000; 2000US-0231266P.  
PR 17-JAN-2001; 2001US-00765101.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA Arap W, Pasqualini R;  
XX WPI; 2002-404697/43.  
DR  
XX Identification of targeting peptides that can be used to treat diseases  
PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis  
PT of Selective Ligands) method comprises a single differential  
PT centrifugation step.  
XX  
PS Example 5; Page 76; 167pp; English.  
XX  
CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis  
CC of Selective Interactive Ligands) to obtain a targeting peptide. The  
CC BRASIL method of the invention involves: exposing a target to a phage  
CC display library in a first phase; exposing the first phase to a second  
CC phase; and separating the phage bound to the target from unbound phage.  
CC The BRASIL method of the invention allows cell phages to be separated  
CC from the remaining unbound phage in a single differential centrifugation  
CC step. When compared to conventional cell panning methods, the BRASIL  
CC method shows a significant increase in recovery of specific phage and a  
CC substantial decrease in background. The BRASIL method is useful for  
CC identifying targeting peptides. The targeting peptides identified by the  
CC method of the invention are useful for treating disease states, such as:  
CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune  
CC disease; bacterial infection; viral infection; cardiovascular disease and  
CC degenerative disease. The present amino acid sequence represents a  
CC targeting peptide of the invention  
XX  
SQ Sequence 9 AA;  
  
Query Match 49.3%; Score 35.5; DB 5; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches		5;	Conservative	2;	Mismatches	2;	Indels	1;	Gaps	1;
QY	1	CGYWLTIWGC	10							
Db	1	CGWW-GLWPC	9							
RESULT 6										
ABJ04460										
ID	ABJ04460	standard; peptide; 9 AA.								
XX	AC	ABJ04460;								
XX	DT	24-OCT-2002 (first entry)								
XX	DE	Stem cell (mesenchymal) targeting peptide 49.								
XX	KW	BRASIL; targeting peptide; bacterial infection;								
XX	KW	Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;								
XX	KW	inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;								
XX	KW	viral infection; cardiovascular disease; degenerative disease.								
XX	OS	Unidentified.								
XX	PN	WO200220822-A2.								
XX	PD	14-MAR-2002.								
XX	PF	07-SEP-2001; 2001WO-US028124.								
XX	PR	08-SEP-2000; 2000US-0231266P.								
XX	PR	17-JAN-2001; 2001US-00765101.								
XX	PA	(TEXA ) UNIV TEXAS SYSTEM.								
XX	PI	Arap W, Pasqualini R;								
XX	XX	WPI; 2002-404697/43.								
DR	XX	Identification of targeting peptides that can be used to treat diseases								
PT	PT	e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis								
PT	PT	of Selective Ligands) method comprises a single differential								
PT	PT	centrifugation step.								
PT	XX	Example 5; Page 76; 167pp; English.								
PS	XX	The invention comprises a method (BRASIL - Biopanning and Rapid Analysis								
XX	CC	of Selective Interactive Ligands) to obtain a targeting peptide. The								
XX	CC	BRASIL method of the invention involves: exposing a target to a phage								
XX	CC	display library in a first phase; exposing the first phase to a second								
XX	CC	phase; and separating the phage bound to the target from unbound phage.								
XX	CC	The BRASIL method of the invention allows cell phages to be separated								
XX	CC	from the remaining unbound phage in a single differential centrifugation								
XX	CC	step. When compared to conventional cell panning methods, the BRASIL								
XX	CC	method shows a significant increase in recovery of specific phage and a								
XX	CC	substantial decrease in background. The BRASIL method is useful for								
XX	CC	identifying targeting peptides. The targeting peptides identified by the								
XX	CC	method of the invention are useful for treating disease states, such as:								
XX	CC	diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune								
XX	CC	disease; bacterial infection; viral infection; cardiovascular disease and								
XX	CC	degenerative disease. The present amino acid sequence represents a								
XX	CC	targeting peptide of the invention								
XX	SQ	Sequence 9 AA;								
Query Match		48.6%;		Score 35;		DB 5;		Length 9;		
Best Local Similarity		50.0%;		Pred. No. 1.7e+06;						
Matches		4;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1	CGYWLTIW	8							
Db	1	CDWWTAW	8							

RESULT 7																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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Db	5	CGYW 8	
RESULT 10			
AAAY76817			
ID	AAAY76817	standard; peptide; 8 AA.	
XX	AC		
XX	AAAY76817;		
DT	28-APR-2000	(first entry)	
XX			
DE	Immunogenic peptide for bi-specific antibody recognition.		
XX			
KW	Immunogenic peptide; bi-specific antibody; diagnosis; immune response;		
KW	diseased tissue identification; therapy.		
XX			
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 1	/note= "acetylated; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"	
FT			
FT	Misc-difference 2	/note= "D-form residue"	
FT	Misc-difference 3	/note= "D-form residue"	
FT	Misc-difference 5	/note= "D-form residue; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"	
FT			
FT	Misc-difference 7	/note= "D-form residue"	
FT	Misc-difference 8	/note= "D-form residue"	
FT			
XX			
PN	WO9966951-A2.		
XX			
PD	29-DEC-1999.		
XX			
PF	22-JUN-1999;	99WO-US013879.	
XX			
PR	22-JUN-1998;	98US-0090142P.	
PR	14-OCT-1998;	98US-0104156P.	
XX			
PA	(IMMU-) IMMUNOMEDICS INC.		
XX			
PI	Hansen HJ,	Griffiths GL, Leung S, McBride WJ, Qu Z;	
XX			
DR	WPI;	2000-160561/14.	
XX			
PT	Bi-specific antibodies that bind specific target tissue and targeted conjugates.		
PT			
XX			
PS	Claim 22;	Page 61; 76pp; English.	
XX			
CC	This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method		
XX			
SQ	Sequence 8 AA;		
Query Match	45.8%;	Score 33;	DB 3; Length 8;
Best Local Similarity	100.0%;	Pred. No. 1.7e+06;	
Matches	4;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	CGYW 4	
Db	5	CGYW 8	
RESULT 11			
ABP53965			
ID	ABP53965	standard; peptide; 8 AA.	
XX			
AC	ABP53965;		
XX			
DT	09-JAN-2003	(first entry)	
XX			
DE	VEGFR-3 binding peptide SEQ ID NO:68.		
XX			
KW	Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnery; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	Misc-difference 4. .6	/note= "X is any amino acid"	
FT	Misc-difference 8	/note= "any amino acid"	
FT			
XX			
PN	WO200257299-A2.		
XX			
PD	25-JUL-2002.		
XX			
PF	16-JAN-2002;	2002WO-IB0000099.	
XX			
PR	17-JAN-2001;	2001US-0262476P.	
XX			
PA	(LUDW-) LUDWIG INST CANCER RES.		
PA	(LICN ) LICENTIA LTD.		
XX			
PI	Alitalo K,	Koivunen E, Kubo H;	
XX			
DR	WPI;	2002-691521/74.	
XX			
PT	New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.		
PT			
XX			
PS	Claim 22;	Page 81; 149pp; English.	
XX			
CC	The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnery activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention		
XX			
SQ	Sequence 8 AA;		



CC polymer conjugate, and administering to the tissue a polymer conjugate  
CC that binds to the capture arm, the polymer conjugate comprising a polymer  
CC conjugated to a diagnostic or therapeutic agent. Also included is a  
CC method for photodynamic diagnosis or treatment of a disease or disorder;  
CC or intravascular or endoscopic method for diagnosing or treating a  
CC disease or disorder. The method is useful for diagnosing or treating a  
CC disease or disorder chosen from cancer (oesophageal, gastric, colonic,  
CC rectal, pancreatic, lung, breast, ovarian, urinary bladder, endometrial,  
CC cervical, testicular, renal, adrenal and liver cancer, solid tumour, B-  
CC cell malignancy or T-cell malignancy); cardiovascular lesion; an  
CC inflammatory disease; neurodegenerative disease; metabolic disease; and  
CC an infectious disease. The B-cell malignancy is chosen from indolent  
CC forms of B-cell lymphomas, aggressive forms of B-cell lymphomas, chronic  
CC lymphatic leukaemias, acute lymphatic leukaemias, and multiple myeloma.  
CC The solid tumour is chosen melanoma, carcinoma (preferably renal  
CC carcinoma, lung carcinoma, intestinal carcinoma, and stomach carcinoma),  
CC glioma and sarcoma. The cardiovascular lesion is chosen from infarct,  
CC clot, embolus, atherosclerotic plaque and ischaemia. The  
CC neurodegenerative disease is Alzheimer's disease. The metabolic disease  
CC is amyloidosis, where the antibody binds amyloid. The disease or disorder  
CC is displaced or ectopic normal tissue chosen from endometrium, thymus,  
CC spleen and parathyroid. The method can be used for normal tissue  
CC ablation, where the tissue is chosen from bone marrow and spleen. The  
CC disease or disorder is an autoimmune disease such as myasthenia gravis,  
CC lupus nephritis, lupus erythematosus, and rheumatoid arthritis, Class III  
CC autoimmune diseases such as immune-mediated thrombocytopenias, such as  
CC acute idiopathic thrombocytopenic purpura and chronic idiopathic  
CC thrombocytopenic purpura, dermatomyositis, Sjogren's syndrome, multiple  
CC sclerosis, Sydenham's chorea, myasthenia gravis, systemic lupus  
CC erythematosus, lupus nephritis, rheumatic fever, polyglandular syndromes,  
CC bullous pemphigoid, diabetes mellitus, Henoch-Schonlein purpura, post-  
CC streptococcal nephritis, erythema nodosum, Takayasu's arteritis,  
CC Addison's disease, rheumatoid arthritis, sarcoidosis, ulcerative colitis,  
CC erythema multiforme, Iga nephropathy, polyarteritis nodosa, ankylosing  
CC spondylitis, Goodpasture's syndrome, thromboangitis obiterans, primary  
CC biliary cirrhosis, Hashimoto's thyroiditis, thyrotoxicosis, scleroderma,  
CC chronic active hepatitis, polymyositis/dermatomyositis, polychondritis,  
CC pemphigus vulgaris, Wegener's granulomatosis, membranous nephropathy,  
CC amyotrophic lateral sclerosis, tabes dorsalis, giant cell  
CC arteritis/polymyalgia, pernicious anaemia, rapidly progressive  
CC glomerulonephritis, or fibrosing alveolitis. The infectious disease is  
CC chosen from bacterial, fungal, parasitic and viral lesion. The infectious  
CC disease is caused by a fungus chosen from Microsporium, Trichophyton,  
CC Epidermophyton, Sporothrix schenckii, Cryptococcus neoformans,  
CC Coccidioides immitis, Histoplasma capsulatum, Blastomyces dermatitidis,  
CC and Candida albicans. The infectious disease is caused by a virus chosen  
CC from HIV, herpes virus, cytomegalovirus, rabies virus, influenza virus,  
CC hepatitis B virus, Sendai virus, feline leukemia virus, Reo virus, polio  
CC virus, human serum parvo-like virus, simian virus 40, respiratory  
CC syncytial virus, mouse mammary tumour virus, Varicella-Zoster virus,  
CC Dengue virus, rubella virus, measles virus, adenovirus, human T-cell  
CC leukemia viruses, Epstein-Barr virus, murine leukemia virus, mumps virus,  
CC vesicular stomatitis virus, Sindbis virus, lymphocytic choriomeningitis  
CC virus, wart virus and blue tongue virus. The infectious disease is caused  
CC by a bacterium chosen from Bacillus anthracis, Streptococcus agalactiae,  
CC Legionella pneumophila, Streptococcus pyogenes, Escherichia coli,  
CC Neisseria gonorrhoeae, Neisseria meningitidis, Pneumococcus, Haemophilus  
CC influenzae B, Treponema pallidum, Lyme disease spirochetes, Pseudomonas  
CC aeruginosa, Mycobacterium leprae , Brucella abortus , Mycobacterium  
CC tuberculosis , and Tetanus toxin . The infectious disease is caused by a  
CC protozoa chosen from Plasmodium falciparum, Plasmodium vivax, Toxoplasma  
CC gondii, Trypanosoma rangeli , Trypanosoma cruzi, Trypanosoma  
CC rhodesiensei, Trypanosoma brucei, Schistosoma mansoni, Schistosoma  
CC japonicum, Babesia bovis, Elmeria tenella, Onchocerca volvulus,  
CC Leishmania tropica, Trichinella spiralis, Onchocerca volvulus, Theileria  
CC parva, Taenia hydatigena, Taenia ovis, Taenia saginata, Echinococcus  
CC granulosa, and Mesocostoides corti. The infectious disease is caused by  
CC a mycoplasma chosen from Mycoplasma arthritis, M. hyorhinis, M. orale,  
CC M. arginini, Acholeplasma laidlawii, M. salivarium and M. pneumoniae. The  
CC cancer is preferably chosen from carcinoembryonic antigen (CEA) -  
CC expressing tumour or a CD20-expressing malignancy. The present sequence  
CC represents a peptide used in the method of the invention.

XX

SQ		Sequence 8 AA;	
Query Match		45.8%; Score 33; DB 8; Length 8;	
Best Local Similarity		100.0%; Pred. No. 1.7e+06;	
Matches		4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	CGYW 4	
Db	5	CGYW 8	
RESULT 14			
ABB46346			
ID	ABB46346 standard; peptide; 10 AA.		
XX	ABB46346;		
AC	ABB46346;		
XX	30-JAN-2002 (first entry)		
DT	Desmoglein-2 CAR sequence cyclic peptide SEQ ID NO 1090.		
XX	Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;		
KW	cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;		
KW	organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.		
XX	Synthetic.		
OS	WO200172956-A2.		
XX	04-OCT-2001.		
PD	27-MAR-2001; 2001WO-IB001400.		
XX	27-MAR-2000; 2000US-00535852.		
PF	(ADHE-) ADHEREX TECHNOLOGIES INC.		
XX	Blaschuk OW, Symonds JM, Gour BJ;		
PI	WPI; 2002-025778/03.		
XX	Modulating agents for inhibiting or enhancing desmosomal cadherin		
PT	mediated cell adhesion, useful for facilitating wound healing and/or		
PPT	reducing scar tissue, treating cancer and inducing apoptosis.		
PT	Claim 18; Page 101; 127pp; English.		
XX	The invention relates to modulating agents for inhibiting or enhancing		
CC	desmosomal cadherin mediated cell adhesion, comprising a modulating agent		
CC	comprising a desmosomal cadherin cell adhesion recognition CAR sequence		
CC	(ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR		
CC	sequence, a substance such as an antibody or antigen-binding fragment		
CC	that specifically binds a desmosomal cadherin CAR sequence and/or a		
CC	polynucleotide encoding a polypeptide that comprises a desmosomal		
CC	cadherin CAR sequence or analogue. The modulating agents have		
CC	immunosuppressive, cytostatic and antiapoptotic activity and are used to		
CC	facilitate wound healing and/or reduce scar tissue, for enhancing		
CC	adhesion of foreign tissue implants (e.g. skin graft or organ implant),		
CC	treating an autoimmune blistering disorder and to treat cancer (e.g.		
CC	carcinoma, leukaemia or melanoma) and induce apoptosis		
XX	Sequence 10 AA;		
SQ		Sequence 10 AA;	
Query Match		45.8%; Score 33; DB 5; Length 10;	
Best Local Similarity		60.0%; Pred. No. 4.6e+02;	
Matches		6; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY	1	CGYWLTIWGC 10	
Db	1	CGYALDARGC 10	
RESULT 15			

ABB46607  
ID ABB46607 standard; peptide; 10 AA.  
XX  
AC ABB46607;  
XX  
DT 30-JAN-2002 (first entry)  
XX  
DE Desmocollin-1 CAR cyclic peptide 9.  
XX  
KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytotatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
XX  
OS Synthetic.  
XX  
PN WO200172956-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 27-MAR-2001; 2001WO-IB001400.  
XX  
PR 27-MAR-2000; 2000US-00535852.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuk OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2002-025778/03.  
XX  
PT Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis.  
XX  
PS Claim 23; Page 109; 127pp; English.  
XX  
CC The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
CC carcinoma, leukaemia or melanoma) and induce apoptosis  
XX  
SQ Sequence 10 AA;  
Query Match 45.8%; Score 33; DB 5; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.6e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CGYWLTIWGC 10  
Db 1 CGYATATADGC 10

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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds  
(without alignments)  
28.022 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	45.8	10	4	US-09-535-852-1090
2	33	45.8	10	4	US-09-535-852-1352
3	30	41.7	8	2	US-08-520-535-12
4	30	41.7	8	2	US-09-079-432-12
5	30	41.7	9	2	US-08-986-234-92
6	30	41.7	9	4	US-09-311-784A-374
7	30	41.7	9	4	US-09-790-497A-1
8	30	41.7	10	3	US-09-108-709-22
9	30	41.7	10	4	US-09-790-497A-110
10	29	40.3	5	1	US-07-946-237-4
11	29	40.3	5	2	US-08-530-566-10
12	29	40.3	5	3	US-09-195-726-10
13	29	40.3	5	3	US-09-067-755-10
14	29	40.3	5	4	US-08-239-765C-4
15	29	40.3	7	4	US-09-069-827A-94
16	29	40.3	9	4	US-09-311-784A-348
17	29	40.3	10	2	US-08-735-253-8
18	29	40.3	10	2	US-08-735-253-13
19	29	40.3	10	3	US-08-481-968A-21
20	29	40.3	10	3	US-08-154-712B-21
21	29	40.3	10	4	US-09-947-925A-21
22	28	38.9	8	3	US-09-315-304B-1649
23	28	38.9	10	1	US-08-250-789A-119
24	28	38.9	10	4	US-09-462-917A-73
25	28	38.9	10	4	US-09-125-641-3
26	28	38.9	10	4	US-09-790-497A-5
27	28	38.9	10	4	US-09-790-497A-24

28	27.5	38.2	6	1	US-08-191-571-12	Sequence 12, Appl
29	27.5	38.2	6	5	PCT-US95-00296-12	Sequence 12, Appl
30	27	37.5	8	3	US-08-925-002-12	Sequence 12, Appl
31	27	37.5	8	3	US-08-586-670A-17	Sequence 17, Appl
32	27	37.5	8	3	US-09-082-279B-1495	Sequence 1495, Ap
33	27	37.5	8	4	US-09-834-784-1495	Sequence 1495, Ap
34	27	37.5	8	4	US-09-910-552-12	Sequence 12, Appl
35	27	37.5	8	4	US-09-350-641C-1650	Sequence 1650, Ap
36	27	37.5	10	3	US-09-315-304B-1587	Sequence 1587, Ap
37	27	37.5	10	4	US-09-350-325-47	Sequence 47, Appl
38	27	37.5	10	4	US-09-535-852-1357	Sequence 1357, Ap
39	27	37.5	10	4	US-09-350-641C-1587	Sequence 1587, Ap
40	27	37.5	10	4	US-09-239-043D-2474	Sequence 2474, Ap
41	27	37.5	10	4	US-09-620-091-28	Sequence 28, Appl
42	27	37.5	10	4	US-09-620-091-42	Sequence 42, Appl
43	27	37.5	10	4	US-09-620-091-47	Sequence 47, Appl
44	26.5	36.8	10	3	US-09-186-958-12	Sequence 12, Appl
45	26.5	36.8	10	3	US-09-669-271A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-535-852-1090  
; Sequence 1090, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1090  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence  
US-09-535-852-1090

Query Match 45.8%; Score 33; DB 4; Length 10;  
Best Local Similarity 60.0%; Pred. No. 81;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
||| |  
Db 1 CGYALDARGC 10

RESULT 2  
US-09-535-852-1352  
; Sequence 1352, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1352  
; LENGTH: 10

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1352

Query Match          45.8%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
      |||||
Db      1 CGYATTADGC 10

RESULT 3
US-08-520-535-12
; Sequence 12, Application US/08520535
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,535
; FILING DATE: 28-AUG-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-520-535-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWL 5
      |||||
Db      1 CDYWL 5

RESULT 4
US-09-079-432-12
; Sequence 12, Application US/09079432
; Patent No. 5955572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,432
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/520,535
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-079-432-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWL 5
      |||||
Db      1 CDYWL 5

RESULT 5
US-08-986-234-92
; Sequence 92, Application US/08986234
; Patent No. 5981706
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-08-986-234-92

Query Match          41.7%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 IWGC 10
      |||||
Db      2 IWGC 5

RESULT 6
US-09-311-784A-374
; Sequence 374, Application US/09311784A
; Patent No. 6534482
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; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/09/311,784A  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 374  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 69 (peptide 25.0113)  
US-09-311-784A-374

Query Match 41.7%; Score 30; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
|||  
Db 1 IWGC 4

RESULT 7

US-09-790-497A-1  
; Sequence 1, Application US/09790497A  
; Patent No. 6649735

; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF  
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING THEM  
; FILE REFERENCE: 2752-16  
; CURRENT APPLICATION NUMBER: US/09/790,497A  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/576,824  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 08/723,425  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: 09/146,028  
; PRIOR FILING DATE: 1993-11-22  
; PRIOR APPLICATION NUMBER: PCT/EP93/00517  
; PRIOR FILING DATE: 1993-03-08  
; PRIOR APPLICATION NUMBER: EP 92400598.6  
; PRIOR FILING DATE: 1992-03-06  
; NUMBER OF SEQ ID NOS: 600  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-790-497A-1

Query Match 41.7%; Score 30; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
|||

Db 1 IWGC 4

RESULT 8

US-09-108-709-22  
; Sequence 22, Application US/09108709  
; Patent No. 6008044

; GENERAL INFORMATION:  
; APPLICANT: Cotropia, Joseph P.  
; TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane Gly  
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (Hiv-1) and Prognosis Test  
; TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibiting  
; TITLE OF INVENTION: Fusion-associated Epitope (GCSGKLIC) in gp-41  
; FILE REFERENCE: 10586/00406  
; CURRENT APPLICATION NUMBER: US/09/108,709  
; CURRENT FILING DATE: 1998-07-01  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(10)  
; OTHER INFORMATION: amino acids 600-609 according to the Gnann  
; OTHER INFORMATION: numbering system

US-09-108-709-22  
Query Match 41.7%; Score 30; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
|||  
Db 1 IWGC 4

RESULT 9

US-09-790-497A-110  
; Sequence 110, Application US/09790497A  
; Patent No. 6649735

; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF  
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING THEM  
; FILE REFERENCE: 2752-16  
; CURRENT APPLICATION NUMBER: US/09/790,497A  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/576,824  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 08/723,425  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: 09/146,028  
; PRIOR FILING DATE: 1993-11-22  
; PRIOR APPLICATION NUMBER: PCT/EP93/00517  
; PRIOR FILING DATE: 1993-03-08  
; PRIOR APPLICATION NUMBER: EP 92400598.6  
; PRIOR FILING DATE: 1992-03-06  
; NUMBER OF SEQ ID NOS: 600  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 110  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-790-497A-110

Query Match 41.7%; Score 30; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
   ||||
Db 1 IWGC 4

RESULT 10
US-07-946-237-4
; Sequence 4, Application US/07946237
; Patent No. 5348874
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,237
; FILING DATE: 19920914
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: David E. Brook
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BTT92-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; MOLECULE TYPE: peptide
US-07-946-237-4

Query Match 40.3%; Score 29; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
   :|||
Db 2 VWGC 5

RESULT 11
US-08-530-566-10
; Sequence 10, Application US/08530566
; Patent No. 5840865
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

Query Match 40.3%; Score 29; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
   :|||
Db 2 VWGC 5

RESULT 12
US-09-195-726-10
; Sequence 10, Application US/09195726
; Patent No. 6159717
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,726
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/530,566
; FILING DATE: 20-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,765
; FILING DATE: 09-MAY-1994
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/946,237  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: IMBB92-01ZAZ  
TELEPHONE: (781) 861-6240  
TELEFAX: (781) 861-9540  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-195-726-10

Query Match 40.3%; Score 29; DB 3; Length 5;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
Db 2 VWGC 5

RESULT 13  
US-09-067-755-10  
Sequence 10, Application US/09067755  
Patent No. 6225121  
GENERAL INFORMATION:  
APPLICANT: Savakis, Charalambos  
APPLICANT: Franz, Gerald H.  
APPLICANT: Loukeris, Athanasios  
APPLICANT: Klinakis, Apostolos G.  
TITLE OF INVENTION: Eukaryotic Transposable Element  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02421  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,755  
FILING DATE: 27-APR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/530,566  
FILING DATE: 20-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/239,765  
FILING DATE: 09-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/946,237  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: IMBB92-01ZAZ  
TELEPHONE: (781) 861-6240  
TELEFAX: (781) 861-9540  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids

TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-067-755-10

Query Match 40.3%; Score 29; DB 3; Length 5;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
Db 2 VWGC 5

RESULT 14  
US-08-239-765C-4  
Sequence 4, Application US/08239765C  
Patent No. 6469228  
GENERAL INFORMATION:  
APPLICANT: Savakis, Charalambos  
APPLICANT: Franz, Gerald H.  
APPLICANT: Loukeris, Athanasios  
TITLE OF INVENTION: Eukaryotic Transposable Element  
FILE REFERENCE: 18747/1130  
CURRENT APPLICATION NUMBER: US/08/239,765C  
CURRENT FILING DATE: 1994-05-09  
PRIOR APPLICATION NUMBER: 07/946,237  
PRIOR FILING DATE: 1992-09-14  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Conserved amino acid sequence of the TC-1 family of transposable  
OTHER INFORMATION: elements  
US-08-239-765C-4

Query Match 40.3%; Score 29; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
Db 2 VWGC 5

RESULT 15  
US-09-069-827A-94  
Sequence 94, Application US/09069827A  
Patent No. 6617114  
GENERAL INFORMATION:  
APPLICANT: FOWLKES, Dana M  
KAY, Brian K  
FRELINGER, Jeffrey A  
HYDE-DERUYSCHE, Robin P  
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING  
COMPLEMENTARY COMBINATORIAL LIBRARIES  
NUMBER OF SEQUENCES: 178  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 624 Ninth Street N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30



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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-Apr-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES=4C
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
;
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-069-827A-94
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Query Match      40.3%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      3 YWLTIWG 9
      ||  ||
Db      1 YWWPDWG 7
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Search completed: December 29, 2004, 21:36:45  
Job time : 24.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:36:53 ; Search time 82 Seconds  
(without alignments)  
43.869 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues 182644  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	13 US-10-046-922-35	Sequence 35, Appl
2	54	75.0	10	13 US-10-046-922-34	Sequence 34, Appl
3	50	69.4	10	13 US-10-046-922-73	Sequence 73, Appl
4	33	45.8	7	13 US-10-046-922-67	Sequence 67, Appl
5	33	45.8	8	13 US-10-046-922-68	Sequence 68, Appl
6	33	45.8	10	17 US-10-654-578-1090	Sequence 1090, Ap
7	33	45.8	10	17 US-10-654-578-1352	Sequence 1352, Ap
8	32	44.4	10	8 US-08-821-739A-90	Sequence 90, Appl
9	32	44.4	10	14 US-10-133-210-39	Sequence 39, Appl
10	32	44.4	10	14 US-10-133-210-69	Sequence 69, Appl
11	31	43.1	9	13 US-10-046-922-36	Sequence 36, Appl
12	31	43.1	10	10 US-09-572-404B-1454	Sequence 1454, Ap
13	30	41.7	9	8 US-08-821-739A-78	Sequence 78, Appl

14	30	41.7	9	9 US-09-832-723-104	Sequence 104, App
15	30	41.7	9	9 US-09-894-018-80	Sequence 80, Appl
16	30	41.7	9	9 US-09-894-018-185	Sequence 185, App
17	30	41.7	9	14 US-10-303-331-104	Sequence 104, App
18	30	41.7	9	14 US-10-371-525-374	Sequence 374, App
19	30	41.7	9	14 US-10-371-069-374	Sequence 374, App
20	30	41.7	9	14 US-10-371-645-374	Sequence 374, App
21	30	41.7	9	14 US-10-371-260-374	Sequence 374, Appl
22	30	41.7	9	17 US-10-474-960A-80	Sequence 80, Appl
23	30	41.7	9	17 US-10-474-960A-185	Sequence 185, App
24	30	41.7	10	15 US-10-462-452-707	Sequence 707, App
25	30	41.7	10	15 US-10-601-953-812	Sequence 812, App
26	30	41.7	10	16 US-10-322-266-708	Sequence 708, App
27	29	40.3	5	8 US-08-239-765B-4	Sequence 4, Appli
28	29	40.3	9	9 US-09-894-018-154	Sequence 154, App
29	29	40.3	9	14 US-10-133-210-8	Sequence 8, Appli
30	29	40.3	9	14 US-10-371-525-348	Sequence 348, App
31	29	40.3	9	14 US-10-371-069-348	Sequence 348, App
32	29	40.3	9	14 US-10-371-645-348	Sequence 348, App
33	29	40.3	9	14 US-10-371-260-348	Sequence 348, App
34	29	40.3	9	15 US-10-182-252A-180	Sequence 180, App
35	29	40.3	9	15 US-10-182-252A-181	Sequence 181, App
36	29	40.3	9	15 US-10-182-252A-305	Sequence 305, App
37	29	40.3	9	15 US-10-182-252A-792	Sequence 792, App
38	29	40.3	9	15 US-10-182-252A-793	Sequence 793, App
39	29	40.3	9	15 US-10-182-252A-837	Sequence 837, App
40	29	40.3	9	15 US-10-182-252A-838	Sequence 838, App
41	29	40.3	9	15 US-10-182-252A-1271	Sequence 1271, Ap
42	29	40.3	9	17 US-10-474-960A-154	Sequence 154, App
43	29	40.3	10	8 US-08-821-739A-92	Sequence 92, Appl
44	29	40.3	10	9 US-09-947-925A-21	Sequence 21, Appl
45	29	40.3	10	14 US-10-094-401-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
; US-10-046-922-35

Query Match 100.0%; Score 72; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
| | | | | | | | | |  
Db 1 CGYWLTIWGC 10

RESULT 2  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki

; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 75.0%; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
|||  
Db 2 GYWLTIWG 9

RESULT 3

US-10-046-922-73  
; Sequence 73, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 73  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: peptide library  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (5)..(7)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-73

Query Match 69.4%; Score 50; DB 13; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
|||  
Db 1 CGYWXXXWXC 10

RESULT 4

US-10-046-922-67  
; Sequence 67, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime

; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X at position 4-6 is any amino acid  
US-10-046-922-67

Query Match 45.8%; Score 33; DB 13; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||  
Db 1 GYWXXXW 7

RESULT 5

US-10-046-922-68  
; Sequence 68, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 68  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-68

Query Match 45.8%; Score 33; DB 13; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||  
Db 1 GYWXXXW 7

RESULT 6

US-10-654-578-1090  
; Sequence 1090, Application US/10654578  
; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: 100086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578

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; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1090
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-10-654-578-1090

Query Match          45.8%; Score 33; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
      |||||
Db      1 CGYALDARGC 10

RESULT 7
US-10-654-578-1352
; Sequence 1352, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1352
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1352

Query Match          45.8%; Score 33; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
      |||||
Db      1 CGYATTADGC 10

RESULT 8
US-08-821-739A-90
; Sequence 90, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
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; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-90

Query Match          44.4%; Score 32; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 LTIWGC 10
      |||||
Db      2 LGIWGC 7

RESULT 9
US-10-133-210-39
; Sequence 39, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-39

Query Match          44.4%; Score 32; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 LTIWGC 10
      |||||
Db      2 LGIWGC 7

RESULT 10
US-10-133-210-69
; Sequence 69, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
```

```
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-69

Query Match      44.4%; Score 32; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 LTIWGC 10
      |||||
Db      2 LGIWGC 7

RESULT 11
US-10-046-922-36
; Sequence 36, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-36

Query Match      43.1%; Score 31; DB 13; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
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Db      2 GYWWDTW 8

RESULT 12
US-09-572-404B-1454
; Sequence 1454, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1454
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in P2RY5 at 139-148 and may interact with Sequen
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; OTHER INFORMATION: in this patent.
US-09-572-404B-1454

Query Match      43.1%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIWG 9
      |||||
Db      1 GWLTVIG 8

RESULT 13
US-08-821-739A-78
; Sequence 78, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-78

Query Match      41.7%; Score 30; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 IWGC 10
      |||||
Db      1 IWGC 4

RESULT 14
US-09-832-723-104
; Sequence 104, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
```



; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 104  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-09-832-723-104

Query Match 41.7%; Score 30; DB 9; Length 9;  
Best Local Similarity 50.0%; Pred. NO. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
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Db 1 CTLWPTFW 8

RESULT 15

US-09-894-018-80  
; Sequence 80, Application US/09894018  
; Patent No. US20020119127A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Denisw  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY  
; FILE REFERENCE: 39963-20033.00  
; CURRENT APPLICATION NUMBER: US/09/894,018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: PCT/US00/35568  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 80  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligopeptide  
US-09-894-018-80

Query Match 41.7%; Score 30; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. NO. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
| | | |  
Db 1 IWGC 4

Search completed: December 29, 2004, 22:01:39  
Job time : 82 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:30:17 ; Search time 19 Seconds  
(without alignments)  
50.640 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	33.3	10	2 S71868	glutathione transf
2	24	33.3	10	2 A35556	hypothetical prote
3	22	30.6	7	2 PT0586	T-cell receptor be
4	22	30.6	10	2 T17075	cytochrome-c oxida
5	21	29.2	10	2 E41946	T-cell receptor ga
6	20	27.8	5	2 JH0253	gut pentapeptide -
7	20	27.8	6	2 F41946	T-cell receptor ga
8	20	27.8	8	2 S19288	acylase - Kluyvera
9	19	26.4	9	2 PT0324	Ig heavy chain CRD
10	19	26.4	10	2 PT0289	Ig heavy chain CRD
11	19	26.4	10	2 E49033	T-cell receptor ga
12	19	26.4	10	2 F49033	T-cell receptor ga
13	19	26.4	10	2 C41946	T-cell receptor ga
14	18	25.0	8	2 JS0315	leucokinin V - Mad
15	18	25.0	10	2 PT0230	Ig heavy chain CDR
16	18	25.0	10	2 PH0923	T-cell receptor be
17	18	25.0	10	2 F33932	Ig mu chain J regi
18	18	25.0	10	4 S14943	UGA3 leader peptid
19	17	23.6	4	2 B53284	T-cell receptor be
20	17	23.6	6	2 PT0629	T-cell receptor be
21	17	23.6	6	2 PT0637	T-cell receptor be
22	17	23.6	6	2 A61068	locustakinin - mig
23	17	23.6	6	4 I79564	hypothetical TCL3
24	17	23.6	7	2 PT0628	T-cell receptor be
25	17	23.6	7	2 PT0642	T-cell receptor be
26	17	23.6	7	2 PT0722	T-cell receptor be
27	17	23.6	7	2 PT0728	T-cell receptor be
28	17	23.6	7	2 PX0008	glucuronosyltransf
29	17	23.6	7	2 B48394	major fat-globule

30	17	23.6	7	2 PD0029	pev-kinin 1 - pena
31	17	23.6	7	2 S57274	triacylglycerol li
32	17	23.6	7	2 S33244	neuromodulatory pe
33	17	23.6	7	2 S33245	neuromodulatory pe
34	17	23.6	7	2 S33246	neuromodulatory pe
35	17	23.6	8	2 PT0724	T-cell receptor be
36	17	23.6	8	2 JS0316	leucokinin VI - Ma
37	17	23.6	8	2 JS0317	leucokinin VII - M
38	17	23.6	8	2 JS0318	leucokinin VIII -
39	17	23.6	8	2 A31570	angiotensin-conver
40	17	23.6	9	2 A24244	adipokinetic hormo
41	17	23.6	9	2 PT0634	T-cell receptor be
42	17	23.6	9	2 PT0562	T-cell receptor be
43	17	23.6	9	2 A60522	sperm-activating p
44	17	23.6	10	2 B33995	hypotrehalosemic h
45	17	23.6	10	2 S08997	hypertrehalosemic

ALIGNMENTS

RESULT 1

S71868

glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)

N;Alternate names: glutathione S-transferase class mu 4

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004

C;Accession: S71868

R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray

A;Reference number: S71864; MUID:96332484; PMID:8760377

A;Accession: S71868

A;Molecule type: protein

A;Residues: 1-10 <ROU>

A;Cross-references: UNIPROT:O7M3E8

C;Comment: At least five species-independent classes of cytosolic glutathion transferases

s mitochondrial form are known.

C;Complex: dimer

C;Function:

A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v

A;Pathway: detoxification; xenobiotics metabolism

A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism

es of damage

C;Superfamily: glutathione transferase

C;Keywords: dimer; transferase

Query Match 33.3%; Score 24; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.9e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 GYW 4

|||

4 GYW 6

Db

RESULT 2

A35556

hypothetical protein (ODC region) - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 30-Sep-1993

C;Accession: A35556

R;Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Dosescu, J.; Almodovar, K.M.; Luk, G.D.

J. Biol. Chem. 265, 4884-4892, 1990

A;Title: Isolation and expression of a human ornithine decarboxylase gene.

A;Reference number: A35556; MUID:90202959; PMID:2318872

A;Accession: A35556

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-10 <MOS>

A;Cross-references: GB:J05271

Query Match

33.3%; Score 24; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 9.9e+02;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYW 4  
| | |  
Db 5 CGAW 8

RESULT 3  
PT0586  
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0586; PT0592  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0586  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)  
C;Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9  
: | | |  
Db 3 SIWG 6

RESULT 4  
T17075  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)  
C;Species: mitochondrion Chamaeleo fischeri  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T17075  
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
J. Mol. Evol. 44, 660-674, 1997  
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene  
A;Reference number: Z18674; MUID:97315309; PMID:9169559  
A;Accession: T17075  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-10 <MAC>  
A;Cross-references: UNIPROT:O79912; EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAC622  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 30.6%; Score 22; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 WLTIW 8  
| | |  
Db 2 WLLRW 6

RESULT 5  
E41946  
T-cell receptor gamma chain (1a.9) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: E41946  
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge  
A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: E41946  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-10 <WHE>  
C;Keywords: T-cell receptor

Query Match 29.2%; Score 21; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWL 5  
| | |  
Db 2 CAVWI 6

RESULT 6  
JH0253  
gut pentapeptide - Japanese eel  
C;Species: Anguilla japonica (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755  
A;Accession: JH0253  
A;Molecule type: protein  
A;Residues: 1-5 <UES>  
A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 27.8%; Score 20; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4  
| : |  
Db 1 GFW 3

RESULT 7  
F41946  
T-cell receptor gamma chain (1a.27) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: F41946  
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge  
A;Reference number: A41946; MUID:92049316; PMID:1658619  
A;Accession: F41946  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-6 <WHE>  
C;Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWL 5  
| | |  
Db 2 CAVWV 6

RESULT 8  
S19288  
acylase - Kluyvera cryocrescens  
C;Species: Kluyvera cryocrescens  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S19288  
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991  
A;Title: Chemical modification of serine at the active site of penicillin acylase from K  
A;Reference number: S19288; MUID:92109664; PMID:1764029  
A;Accession: S19288  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <NAR>  
A;Cross-references: UNIPROT:Q7M124

Query Match 27.8%; Score 20; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWL 5  
| | |  
Db 1 CNMWV 5

RESULT 9  
PT0324  
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0324  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0324  
A;Molecule type: DNA  
A;Residues: 1-9 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.4%; Score 19; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | | |  
Db 3 GYGESYW 9

RESULT 10  
PT0289  
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0289  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0289  
A;Molecule type: DNA  
A;Residues: 1-10 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 5.4e+03;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIWG 9  
| | | | |  
Db 4 WISMGG 9

RESULT 11  
E49033  
T-cell receptor gamma chain V-D-J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 25-Aug-1995 #text\_change 21-Jul-2000

C;Accession: E49033; D49033  
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
Eur. J. Immunol. 21, 2999-3007, 1991  
A;Title: Functionally distinct subsets of human gamma/delta T cells.  
A;Reference number: A49033; MUID:92083926; PMID:1684157  
A;Accession: E49033  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-10 <MOR>  
A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697  
A;Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)  
A;Accession: D49033  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-10 <MOR2>  
A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697  
A;Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)  
C;Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYW 4  
| | |  
Db 1 CALW 4

RESULT 12  
F49033  
T-cell receptor gamma chain V-D-J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C;Accession: F49033  
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
Eur. J. Immunol. 21, 2999-3007, 1991  
A;Title: Functionally distinct subsets of human gamma/delta T cells.  
A;Reference number: A49033; MUID:92083926; PMID:1684157  
A;Accession: F49033  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-10 <MOR>  
A;Cross-references: GB:S72605; NID:g240700; PIDN:AAB20632.1; PID:g240701  
A;Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIP:72606)  
C;Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYW 4  
| | |  
Db 1 CALW 4

RESULT 13  
C41946  
T-cell receptor gamma chain (1t.60) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: C41946  
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger  
A;Reference number: A41946; MUID:92049316; PMID:1658619  
A;Accession: C41946  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-10 <WHE>  
C;Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.4e+03;



Matches	2;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	CGYW 4							
Db	2	CAVW 5							
RESULT 14									
JS0315									
leucokinin V - Madeira cockroach									
C;Species: Leucophaea maderae (Madeira cockroach)									
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004									
C;Accession: JS0315									
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.									
Comp. Biochem. Physiol. C 88, 27-30, 1987									
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic									
A;Reference number: JS0315									
A;Accession: JS0315									
A;Molecule type: protein									
A;Residues: 1-8 <HOL>									
A;Cross-references: UNIPROT:P19987									
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act									
C;Keywords: amidated carboxyl end; cephalomyotropic peptide									
F;8/Modified site: amidated carboxyl end (Gly) #status experimental									
Query Match 25.0%; Score 18; DB 2; Length 8;									
Best Local Similarity 37.5%; Pred. No. 2.8e+05;									
Matches	3;	Conservative	1;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	2	GYWLTWIG 9							
			:	:					
Db	1	GSGFSSWG 8							
RESULT 15									
PT0230									
Ig heavy chain CDR3 region (clone 1-118A) - human (fragment)									
C;Species: Homo sapiens (man)									
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996									
C;Accession: PT0230									
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.									
J. Exp. Med. 173, 395-407, 1991									
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j									
A;Reference number: PT0222; MUID:91108337; PMID:1899102									
A;Accession: PT0230									
A;Molecule type: DNA									
A;Residues: 1-10 <YAM>									
A;Experimental source: B lymphocyte									
C;Keywords: heterotetramer; immunoglobulin									
Query Match 25.0%; Score 18; DB 2; Length 10;									
Best Local Similarity 60.0%; Pred. No. 7.5e+03;									
Matches	3;	Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	5	LTWIG 9							
		: :							
Db	3	ITIFG 7							

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OM protein - protein search, using sw model  
Run on: December 29, 2004, 21:27:57 ; Search time 100 Seconds  
(without alignments)  
57.537 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 GYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.5	42.4	10	1 LABA JATMU	P13270 Jatropha mu
2	27	37.5	10	2 Q8SHF6	Q8shf6 chamaeleo m
3	26	36.1	8	2 Q70Y57	Q70y57 fuerstia af
4	26	36.1	8	2 CAD45547	Cad45547 fuerstia
5	24	33.3	10	2 Q7M3E8	Q7m3e8 sus scrofa
6	24	33.3	10	2 Q8SHN1	Q8shn1 bradypodion
7	24	33.3	10	2 Q6JL97	Q6jl97 neisseria g
8	24	33.3	10	2 AAS16521	Aas16521 neisseria
9	23.5	32.6	9	2 Q85DB0	Q85db0 lepitemur s
10	23.5	32.6	9	2 Q85DB8	Q85db8 lepitemur e
11	23.5	32.6	9	2 Q94NA9	Q94na9 daubentonio
12	23.5	32.6	9	2 Q94NB0	Q94nb0 microcebus
13	23.5	32.6	9	2 Q94NB1	Q94nb1 microcebus
14	23.5	32.6	9	2 Q94NB2	Q94nb2 microcebus
15	23.5	32.6	9	2 Q94XE6	Q94xe6 tectocoris
16	23	31.9	10	2 Q8SHC6	Q8shc6 furcifer be
17	22	30.6	10	2 Q79912	Q79912 chamaeleo f
18	22	30.6	10	2 Q9G697	Q9g697 chamaeleo d
19	22	30.6	10	2 Q8SH83	Q8sh83 brookesia t
20	22	30.6	10	2 Q8SH85	Q8sh85 brookesia t
21	22	30.6	10	2 Q8SH88	Q8sh88 brookesia t
22	22	30.6	10	2 Q8SH90	Q8sh90 brookesia s
23	22	30.6	10	2 Q8SH96	Q8sh96 brookesia p
24	22	30.6	10	2 Q8SHA2	Q8sha2 brookesia b
25	22	30.6	10	2 Q8SHA5	Q8sha5 brookesia a
26	22	30.6	10	2 Q8SHC9	Q8shc9 furcifer ba
27	22	30.6	10	2 Q8SHD2	Q8shd2 chamaeleo w
28	22	30.6	10	2 Q8SHD5	Q8shd5 chamaeleo s
29	22	30.6	10	2 Q8SHD8	Q8shd8 chamaeleo r
30	22	30.6	10	2 Q8SHE1	Q8she1 chamaeleo q
31	22	30.6	10	2 Q8SHE4	Q8she4 chamaeleo q

32	22	30.6	10	2 Q8SHE7	Q8she7 chamaeleo p
33	22	30.6	10	2 Q8SHF3	Q8shf3 chamaeleo m
34	22	30.6	10	2 Q8SHF9	Q8shf9 chamaeleo j
35	22	30.6	10	2 Q8SHG5	Q8shg5 chamaeleo h
36	22	30.6	10	2 Q8SHG8	Q8shg8 chamaeleo g
37	22	30.6	10	2 Q8SHH1	Q8shh1 chamaeleo f
38	22	30.6	10	2 Q8SHH4	Q8shh4 chamaeleo e
39	22	30.6	10	2 Q8SHH7	Q8shh7 chamaeleo e
40	22	30.6	10	2 Q8SHI0	Q8shi0 chamaeleo d
41	22	30.6	10	2 Q8SHI3	Q8shi3 chamaeleo c
42	22	30.6	10	2 Q8SHI6	Q8shi6 chamaeleo c
43	22	30.6	10	2 Q8SHI9	Q8shi9 chamaeleo c
44	22	30.6	10	2 Q8SHJ2	Q8shj2 chamaeleo a
45	22	30.6	10	2 Q8SHJ5	Q8shj5 calumma par

ALIGNMENTS

RESULT 1  
LABA\_JATMU  
ID LABA\_JATMU STANDARD; PRT; 10 AA.  
AC P13270;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Labaditin.  
OS Jatropha multifida (Physic nut).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaeae;  
OC Jatropha.  
OX NCBI\_TaxID=3996;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Latex;  
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;  
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha  
multifida L. (Euphorbiaceae). Isolation and sequence determination by  
means of two-dimensional NMR.";  
RL FEBS Lett. 256:91-96(1989).  
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the  
classical pathway of complement activation in vitro. Activity  
seems to be based on an interaction with C1.  
CC -!- PTM: This is a cyclic peptide.  
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine  
for treatment of infected wounds, skins infections and scabies.  
KW Direct protein sequencing.  
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 42.4%; Score 30.5; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 5.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
QY 2 GYWLTIWG 9  
Db 2 GYW-TVWG 8

RESULT 2  
Q8SHF6  
ID Q8SHF6 PRELIMINARY; PRT; 10 AA.  
AC Q8SHF6;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Chamaeleo melleri (Meller's chameleon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.  
OX NCBI\_TaxID=179915;

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169767; PubMed=12182400;
RA Townsend T., Larson A.;
RT "Molecular phylogenetics and mitochondrial genomic evolution in the
RT chamaeleonidae (Reptilia, Squamata).";
RL Mol. Phylogenet. Evol. 23:22-36(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448755; AAL90547.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1276 MW; 5E218E2733772727 CRC64;

Query Match 37.5%; Score 27; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIW 8
Db 2 WLLW 6

RESULT 3
Q70Y57
ID Q70Y57 PRELIMINARY; PRT; 8 AA.
AC Q70Y57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rps16;
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
Db 2 TIWG 5

RESULT 4
CAD45547
ID CAD45547 PRELIMINARY; PRT; 8 AA.
AC CAD45547;
DT 14-MAR-2004 (TrEMBLrel. 27, Created)
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
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GN RPS16.
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
Db 2 TIWG 5

RESULT 5
Q7M3E8
ID Q7M3E8 PRELIMINARY; PRT; 10 AA.
AC Q7M3E8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE.
RA Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
RT "Characterization of pig liver glutathione S-transferases using HPLC-
RT electrospray-ionization mass spectrometry.";
RL Biochem. J. 317:879-884(1996).
DR PIR; S71868; S71868.
DR GO; GO:0004364; F:glutathione transferase activity; IEA.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1223 MW; 5E16395AB36B5877 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4
Db 4 GYW 6

RESULT 6
Q8SHN1
ID Q8SHN1 PRELIMINARY; PRT; 10 AA.
AC Q8SHN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bradypodion taitanum (Dwarf Fischer's chameleon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



Q85DB8  
ID Q85DB8 PRELIMINARY; PRT; 9 AA.  
AC Q85DB8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Lepilemur edwardsi (Milne-Edwards's sportive lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.  
OX NCBI\_TaxID=122230;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).  
DR EMBL; AF224595; AAP33644.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 32.6%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db || ||  
5 YW---WG 8  
  
RESULT 11  
Q94NA9  
ID Q94NA9 PRELIMINARY; PRT; 9 AA.  
AC Q94NA9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Daubentonia madagascariensis (Aye-aye).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentonidae;  
OC Daubentonia.  
OX NCBI\_TaxID=31869;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22281620; PubMed=12393004;  
RA Pastorini J., Forstner M.R., Martin R.D.;  
RT "Phylogenetic relationships among Lemuridae (Primates): evidence from mtDNA.";  
RL J. Hum. Evol. 43:463-478 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).  
DR EMBL; AF224641; AAK70615.1; -.  
DR EMBL; AF224642; AAK70619.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 32.6%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db || ||  
5 YW---WG 8  
  
RESULT 12  
Q94NB0  
ID Q94NB0 PRELIMINARY; PRT; 9 AA.  
AC Q94NB0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus rufus (Brown mouse lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
OC Microcebus.  
OX NCBI\_TaxID=122232;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).  
DR EMBL; AF224636; AAK70595.1; -.  
DR EMBL; AF224637; AAK70599.1; -.  
DR EMBL; AF224638; AAK70603.1; -.  
DR EMBL; AF224639; AAK70607.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 32.6%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db || ||  
5 YW---WG 8  
  
RESULT 13  
Q94NB1  
ID Q94NB1 PRELIMINARY; PRT; 9 AA.  
AC Q94NB1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus ravelobensis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
OC Microcebus.  
OX NCBI\_TaxID=122231;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)  
RT based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy  
RT lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224630; AAK70571.1; -.  
DR EMBL; AF224631; AAK70575.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
  
Query Match 32.6%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db || ||  
5 YW---WG 8  
  
RESULT 14  
Q94NB2 ID Q94NB2 PRELIMINARY; PRT; 9 AA.  
AC Q94NB2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus murinus (Lesser mouse lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
OC Microcebus.  
OX NCBI\_TaxID=30608;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)  
RT based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy  
RT lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224624; AAK70547.1; -.  
DR EMBL; AF224625; AAK70551.1; -.  
DR EMBL; AF224626; AAK70555.1; -.  
DR EMBL; AF224627; AAK70559.1; -.  
DR EMBL; AF224628; AAK70563.1; -.  
DR EMBL; AF224629; AAK70567.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 3 YWLTWIG 9  
Db || ||  
5 YW---WG 8  
  
RESULT 15  
Q94XE6 ID Q94XE6 PRELIMINARY; PRT; 9 AA.  
AC Q94XE6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit III (Fragment).  
GN Name=cox3;  
OS Tectocoris diophthalmus (cotton harlequin bug).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;  
OC Tectocoris.  
OX NCBI\_TaxID=159956;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396409; PubMed=11504862;  
RA Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;  
RT "Increased rate of gene rearrangement in the mitochondrial genomes of  
RT three orders of hemipteroid insects.";  
RL Mol. Biol. Evol. 18:1828-1832(2001).  
DR EMBL; AF335990; AAK55283.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;  
  
Query Match 32.6%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
Qy 3 YWLTWIG 9  
Db || ||  
5 YW---WG 8  
  
Search completed: December 29, 2004, 21:41:52  
Job time : 100 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 69.6226 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	5	ABP53932 VEGFR-3 b
2	54	75.0	10	5	ABP53931 VEGFR-3 b
3	50	69.4	10	5	ABP53968 VEGFR-3 b
4	47.5	66.0	304	7	ADC87481 Human GPC
5	47	65.3	25	7	ADC99638 Cancer-re
6	46	63.9	17	6	Aao26074 Fc region
7	46	63.9	17	8	Adj50741 Human ser
8	46	63.9	136	8	Adm87650 Human EST
9	45	62.5	129	5	Aau90545 Insulin/i
10	45	62.5	129	2	Aay59880 Human nor
11	45	62.5	828	6	Abu49938 Protein e
12	44.5	61.8	1024	5	Abb04861 LDL recep
13	44	61.1	149	8	Adp29850 Human sec
14	44	61.1	166	6	Aae31487 Human but
15	44	61.1	415	5	Aau91293 Human NOV
16	43	59.7	13	6	Aao26093 Fc region
17	43	59.7	13	8	Adj50760 Human ser
18	43	59.7	454	5	Abp73979 Candida a
19	43	59.7	474	6	Abu30004 Protein e
20	43	59.7	492	7	ADC97318 E. faeciu
21	43	59.7	1084	8	Adl1869 P. aerugi
22	42.5	59.0	152	3	Aay94989 Human sec
23	42.5	59.0	152	5	Abb90081 Human pol
24	42.5	59.0	152	5	Aao17173 Human sec
25	42.5	59.0	152	5	Abg64784 Human alb

26	42.5	59.0	152	8	ADL78051	Adl78051 Albumin f
27	42.5	59.0	159	2	AAR66278	Aar66278 Therapeut
28	42.5	59.0	159	3	AAB12156	Aab12156 Hydrophob
29	42.5	59.0	159	4	AAM78581	Aam78581 Human pro
30	42.5	59.0	159	4	AAB73100	Aab73100 Human ang
31	42.5	59.0	159	5	AAO17198	Aao17198 Human sec
32	42.5	59.0	159	5	ABG64785	Abg64785 Human alb
33	42.5	59.0	159	8	ADL78052	Adl78052 Albumin f
34	42.5	59.0	159	8	ADN05188	Adn05188 Antipsori
35	42.5	59.0	161	4	AAM25822	Aam25822 Human pro
36	42.5	59.0	161	4	ABB12006	Abb12006 Human gli
37	42.5	59.0	161	4	AAM79565	Aam79565 Human pro
38	42.5	59.0	176	6	ABO07116	Abo07116 Novel hum
39	42.5	59.0	1024	5	ABB04863	Abb04863 LDL recep
40	42.5	59.0	1765	2	AAY16572	Aay16572 Type 5 so
41	42.5	59.0	1765	2	AAY41668	Aay41668 Rat senso
42	42.5	59.0	1765	2	AAY06596	Aay06596 Rat sodiu
43	42.5	59.0	1765	4	AAB20122	Aab20122 Rat sodiu
44	42.5	59.0	1765	4	AAB20123	Aab20123 Rat sodiu
45	42.5	59.0	1765	7	ADD32192	Add32192 Rat Na v

ALIGNMENTS

RESULT 1  
ABP53932  
ID ABP53932 standard; peptide; 10 AA.  
XX  
AC ABP53932;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:35.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.

16-JAN-2002; 2002WO-IB0000099.  
17-JAN-2001; 2001US-0262476P.  
(LUDW-) LUDWIG INST CANCER RES.  
(LICN ) LICENTIA LTD.  
PI Alitalo K, Koivunen E, Kubo H;  
XX WPI; 2002-691521/74.  
DR  
XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 13; Page 80; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnery activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 100.0%; Score 72; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGYWLTIWGC 10  
Db 1 CGYWLTIWGC 10  
| | | | | | | | | |  
  
RESULT 2  
ABP53931  
ID ABP53931 standard; peptide; 10 AA.  
XX  
AC ABP53931;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:34.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "any amino acid"  
FT Misc-difference 10 /note= "any amino acid"  
FT  
XX WO200257299-A2.  
PN  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 12; Page 80; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnery activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 75.0%; Score 54; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
Db 2 GYWLTIWG 9  
| | | | | | | | | |  
  
RESULT 3  
ABP53968  
ID ABP53968 standard; peptide; 10 AA.  
XX  
AC ABP53968;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:73.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 5. .7 /note= "X is any amino acid"  
FT Misc-difference 9 /note= "X is any amino acid"  
FT  
XX WO200257299-A2.  
PN  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Disclosure; Page 147; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnery activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a VEGFR-3 binding peptide, which is given in the  
CC exemplification of the present invention

XX SQ Sequence 10 AA;

Query Match 69.4%; Score 50; DB 5; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10  
|||||  
Db 1 CGYWXWXC 10

RESULT 4

ADC87481  
ID ADC87481 standard; protein; 304 AA.

XX AC ADC87481;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR protein SEQ ID NO:1934.

XX KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
KW gene therapy.

XX OS Homo sapiens.

XX PN EP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002EP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

DR N-PSDB; ADC87480.

XX PT New polynucleotide, useful for preparing a composition for treating a  
PT patient in need of increased or suppressed activity or expression of the  
PT guanosine triphosphate-binding protein coupled receptor.

XX PS Claim 2; SEQ ID NO 1934; 28pp; English.

XX CC The invention relates to a novel polynucleotide encoding a guanosine  
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
CC the invention may have a use in gene therapy. The polynucleotide and  
CC polypeptide are useful for preparing a composition for treating a patient  
CC in need of increased or suppressed activity or expression of the  
CC guanosine triphosphate-binding protein coupled receptor. The protein  
CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.

XX SQ Sequence 304 AA;

Query Match 66.0%; Score 47.5; DB 7; Length 304;  
Best Local Similarity 60.0%; Pred. No. 91;  
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CGYWLTIWGC 10  
|||||  
Db 108 CGFW-AWGC 116

RESULT 5

ADC99638  
ID ADC99638 standard; peptide; 25 AA.

XX AC ADC99638;

XX DT 01-JAN-2004 (first entry)

XX DE Cancer-related Tie-1-binder peptide - SEQ ID 476.

XX KW cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;  
KW leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;  
KW VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;  
KW kinase insert domain protein receptor; EGFR; epidermal growth factor;  
KW FGFR1; fibroblast growth factor; Tie-1.

XX OS Unidentified.

XX PN WO2003035839-A2.

XX PD 01-MAY-2003.

XX PF 24-OCT-2002; 2002WO-US034021.

XX PR 24-OCT-2001; 2001US-0345471P.

XX PA (DGIB-) DGI BIOTECHNOLOGIES INC.

PI Pillutla RC, Brissette R, Spruyt M, Dedova O, Blume A;

PI Prendergast J, Goldstein N;

XX WPI; 2003-457332/43.

XX DR Selecting target and target binder pairs for preparing a composition for  
XX treating cancer by mixing in a reaction vessel. phage expressing  
XX biological targets and phage expressing target binders.

XX PS Claim 26; SEQ ID NO 476; 172pp; English.

XX CC The invention relates to a novel method of selecting target and target  
CC binder pairs comprising mixing in a reaction vessel phage expressing  
CC biological targets and phage expressing target binders, each having  
CC distinguishable selection markers and selecting target and target binder  
CC pairs based on the selection markers. The molecules of the invention  
CC demonstrate cytostatic activity whilst the method may be useful for  
CC selecting target and target binder pairs for preparing a composition for  
CC treating cancer. Furthermore, the method may be utilised during gene  
CC therapy procedures. The current sequence is that of the cancer-related  
CC Tie1-binder peptide of the invention.

XX SQ Sequence 25 AA;

Query Match 65.3%; Score 47; DB 7; Length 25;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 9  
|||||  
Db 5 CGYWGELWGC 13

RESULT 6

AAO26074  
ID AAO26074 standard; peptide; 17 AA.

XX AC AAO26074;

XX DT 03-APR-2003 (first entry)

XX DE Fc region binding peptide SEQ ID No 54.

XX XX



KW Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;  
KW antibody response; half-life; stability; circulatory system.  
XX Unidentified.  
OS WO200286070-A2.  
XX 31-OCT-2002.  
PD 18-APR-2002; 2002WO-US012492.  
XX 18-APR-2001; 2001US-0284534P.  
XX (DYAX-) DYAX CORP.  
XX Rondon IJ, Wu Q, Ley AC, Stochl M, Ranschoff TC, Potter MD;  
PI WPI; 2003-201220/19.  
XX New polypeptides, useful as binding molecules for detecting, isolating or  
PT purifying immunoglobulin Fc-region polypeptides present in a solution, or  
PT for regulating or preventing an antibody response.  
XX Claim 3; Page 76; 152pp; English.  
PS The invention relates to novel isolated polypeptides comprising a  
XX sequence that binds an immunoglobulin Fc region. The polypeptides are  
CC useful as binding molecules for detecting, isolating or purifying  
CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole  
CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are  
CC also useful for regulating or preventing an antibody response, or for  
CC increasing the half-life and over all stability of a therapeutic or  
CC diagnostic compound that is administered to or enters the circulatory  
CC system of an individual. This sequence represents an Fc region binding  
CC peptide of the invention  
XX Sequence 17 AA;  
SQ Query Match 63.9%; Score 46; DB 6; Length 17;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CGYWLTIWG 9  
Db ||:| |||  
4 CGFWPRIWG 12  
RESULT 7  
ADJ50741  
ID ADJ50741 standard; peptide; 17 AA.  
XX AC ADJ50741;  
XX 06-MAY-2004 (first entry)  
DT Human serum albumin binding peptide, Seq ID No 278.  
DE human serum albumin; HSA; serum; blood; tumour; human.  
XX Homo sapiens.  
OS WO2003106493-A1.  
XX 24-DEC-2003.  
PD 16-JUN-2003; 2003WO-US018896.  
XX 14-JUN-2002; 2002US-0388642P.  
XX (DYAX-) DYAX CORP.  
PA Sato AK, Dawson BM;  
PI New isolated polynucleotides and polypeptides, useful for treating, e.g.  
XX

DR WPI; 2004-082161/08.  
XX Evaluating sample comprising soluble serum protein by forming complex  
PT comprising serum protein and physically associated compounds using  
PT peptide ligand that specifically binds with proteins, which is separated  
PT and evaluated.  
XX Disclosure; SEQ ID NO 278; 191pp; English.  
PS The invention relates to a method of evaluating sample by providing a  
XX soluble serum protein (I), one or more compounds physically associated  
CC with (I), and a (I)-binding agent that comprises a peptide that  
CC specifically binds to (I), allowing the (I)-binding agent to bind to (I)  
CC to form a complex including one or more compounds physically associated  
CC with (I), separating the complex from one or more components of the  
CC sample, and evaluating one or more of the physically associated  
CC compounds. The sample comprises blood or serum, or is obtained from a  
CC biopsy. The sample may also be obtained from a tumour or a region within  
CC 5 mm of a tumour. The method is useful for detecting modulators that  
CC modulate interaction of serum protein-binding compound and serum protein  
CC and for identifying binding ligands for serum protein. The present  
CC sequence represents a serum albumin-binding peptide identified using the  
CC method of the invention.  
XX Sequence 17 AA;  
SQ Query Match 63.9%; Score 46; DB 8; Length 17;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CGYWLTIWG 9  
Db ||:| |||  
4 CGFWPRIWG 12  
RESULT 8  
ADM87650  
ID ADM87650 standard; protein; 136 AA.  
XX AC ADM87650;  
XX 03-JUN-2004 (first entry)  
DT Human EST derived amino acid sequence SEQ ID NO:743.  
XX respiratory; cytostatic; antiarthritic; antiinflammatory;  
DE gastrointestinal; antibacterial; immunosuppressive; antidiabetic;  
KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;  
KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;  
KW inflammatory condition; arthritis; inflammatory bowel disease;  
KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;  
KW graft versus host disease; human; expressed sequence tag; EST.  
XX Homo sapiens.  
OS WO2004009834-A2.  
XX 29-JAN-2004.  
PD 19-JUL-2002; 2002WO-US022858.  
PF 21-JUL-2001; 2001US-0306971P.  
XX 28-MAR-2002; 2002US-00112944.  
PR (NUVE-) NUVELO INC.  
XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;  
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;  
XX WPI; 2004-143291/14.  
DR N-PSDB; ADM87432.  
XX New isolated polynucleotides and polypeptides, useful for treating, e.g.  
PT

PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,  
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft  
PT versus host disease.  
XX  
PS Example 2; SEQ ID NO 743; 591pp; English.  
XX  
CC The present invention describes an isolated polynucleotide (I): (a)  
CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)  
CC which encodes a polypeptide with biological activity, where the  
CC polynucleotide hybridises to (i) under stringent hybridisation conditions  
CC or has greater than 99% sequence identity with (i). (i) has respiratory,  
CC cytostatic, antiarthritic, antiinflammatory, gastrointestinal,  
CC antibacterial, immunosuppressive, antidiabetic and antirheumatic  
CC activities, and can be used in gene therapy. (i) can be used for  
CC generating polynucleotides encoding chimeric or fusion proteins and  
CC heterologous protein sequences. The polynucleotides can be used to  
CC express recombinant protein for analysis, characterisation or therapeutic  
CC use; as markers for tissues in which the corresponding protein is  
CC preferentially expressed; as molecular weight markers on gels; as  
CC chromosome markers or tags to identify chromosomes or to map related gene  
CC positions; to compare with endogenous DNA sequences in patients to  
CC identify potential genetic disorders; as probes to hybridise and discover  
CC genes, related DNA sequences; as a source of information to derive PCR  
CC primers for genetic fingerprinting; as a probe to subtract-out known  
CC sequences in the process of discovering other novel polynucleotides; for  
CC selecting and making oligomers for attachment to a gene chip or other  
CC support, including for examination of expression patterns; to raise anti-  
CC protein antibodies using DNA immunisation techniques; and as an antigen  
CC to raise anti-DNA antibodies or elicit another immune response. The  
CC polynucleotides and polypeptides can also be used as nutritional sources  
CC or supplements, e.g. as a protein or amino acid supplement, as a carbon  
CC source, as a nitrogen source or as a source of carbohydrates. The  
CC polynucleotides and polypeptides can also be used treat cancer. The  
CC compositions are useful for promoting better or faster closure of non-  
CC healing wounds, for the generation and regeneration of tissues, for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues, and conditions resulting from  
CC systemic cytokine damage. The compositions can also be used to treat  
CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or  
CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1  
CC or graft versus host disease. The present sequence represents an  
CC expressed sequence tag (EST) derived amino acid sequence from the present  
CC invention. N.B. The sequences for this patent were obtained from the  
CC USPTO web site from an equivalent US patent US20040048249A1.  
XX  
SQ Sequence 136 AA;  
  
Query Match 63.9%; Score 46; DB 8; Length 136;  
Best Local Similarity 60.0%; Pred. No. 73;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 CGYWLTIWGC 10  
Db 93 CGRWDWLWGC 102  
  
RESULT 9  
AAU90545  
ID AAU90545 standard; peptide; 20 AA.  
XX  
AC AAU90545;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Insulin/insulin-like growth factor receptor-binding peptide #2501.  
XX  
KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;  
KW ophthalmological; insulin; receptor; gene therapy; diabetes;  
KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;  
KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.  
XX  
OS Synthetic.  
XX

PN WO200172771-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 29-MAR-2000; 2000WO-US008528.  
XX  
PR 29-MAR-2000; 2000WO-US008528.  
XX  
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
PA (NOVO ) NOVO NORDISK AS.  
XX  
PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;  
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;  
PI Hansen PH, Ravera M, Hsiao K;  
XX WPI; 2002-025774/03.  
DR  
XX Modulating insulin activity in mammalian cells, for treating e.g.  
PT diabetes and tumors, comprises using peptides that bind to insulin or  
PT insulin-like growth factor receptors.  
XX  
PS Disclosure; Fig 8-3; 390pp; English.  
XX  
CC The invention relates to a method of modulating insulin activity in  
CC mammalian cells by administering a peptide that binds the insulin  
CC receptor (IR). A composition containing a peptide, optionally expressed  
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin  
CC agonist are useful for treating diabetes. Also, peptides that are  
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are  
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours  
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1  
CC receptor agonists are useful for treating neurological diseases,  
CC including stroke and diabetic neuropathy. The peptides are also useful in  
CC screening for compounds that bind to IR or IGF-1 receptor, potential  
CC therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or  
CC IGF-1 receptor-binding peptides and related amino acid sequences of the  
CC invention  
XX  
SQ Sequence 20 AA;  
  
Query Match 62.5%; Score 45; DB 5; Length 20;  
Best Local Similarity 60.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 CGYWLTIWGC 10  
Db 8 CGAWPTYWNC 17  
  
RESULT 10  
AAY59880  
ID AAY59880 standard; protein; 129 AA.  
XX  
AC AAY59880;  
XX  
DT 19-JAN-2000 (first entry)  
XX  
DE Human normal uterus tissue derived protein 43.  
XX  
KW Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;  
KW EST; expressed sequence tag.  
XX  
OS Homo sapiens.  
XX  
PN DE19817946-A1.  
XX  
PD 21-OCT-1999.  
XX  
PF 17-APR-1998; 98DE-01017946.  
XX  
PR 17-APR-1998; 98DE-01017946.  
XX  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
XX DR WPI; 1999-591956/51.  
DR N-PSDB; AAZ41339.  
XX PT New nucleic acid sequences expressed in normal uterine tissues, and  
PT derived polypeptides, for treatment of uterine cancer and identification  
PT of therapeutic agents.  
XX PS Claim 23; Page 138; 154pp; German.  
XX CC This invention describes novel cDNA sequences (A) highly expressed in  
CC normal uterine tissue which can have anticancer and cytostatic activity  
CC and can be used for gene therapy. (A) are used (i) for recombinant  
CC expression of polypeptides (B) and (ii) to isolate complete genes. (B)  
CC are used (i) to identify agents suitable for treatment of uterine cancer;  
CC (ii) directly for treating this form of cancer (including expression from  
CC gene therapy vectors) and (iii) for generation of specific antibodies.  
CC (A) are identified by assembling ESTs (expressed sequence tags) from a  
CC particular tissue type before comparison of expression patterns. This  
CC allows a significantly longer fragment of the gene to be revealed, so  
CC should reduce the number of failures associated with the fact that ESTs  
CC from different libraries may represent different parts of the same  
CC unknown gene, distorting the estimated frequency of occurrence in a  
CC particular tissue. AAY59838-Y59892 represent protein fragments encoded by  
CC the human uterine tissue derived cDNA fragments represented in AAZ41325-  
CC Z41385  
XX SQ Sequence 129 AA;  
Query Match 62.5%; Score 45; DB 2; Length 129;  
Best Local Similarity 62.5%; Pred. No. 96;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CGYWLTIW 8  
| : ||| : |  
Db 32 CSHWLTWV 39  
RESULT 11  
ABU49938  
ID ABU49938 standard; protein; 828 AA.  
XX AC ABU49938;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by prokaryotic essential gene #35465.  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Yersinia pestis.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX DR WPI; 2003-029926/02.  
DR N-PSDB; ACA53808.

XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 77862; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 828 AA;  
Query Match 62.5%; Score 45; DB 6; Length 828;  
Best Local Similarity 58.3%; Pred. No. 4.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
QY 1 CGYWLTI--WGC 10  
| | | | : | | |  
Db 372 CGLWLELLSWG 383  
RESULT 12  
ABB04861  
ID ABB04861 standard; protein; 1024 AA.  
XX AC ABB04861;  
XX DT 13-MAR-2002 (first entry)  
XX DE LDL receptor binding protein Na channel brain 3 SEQ ID NO:84.  
XX KW Low density lipoprotein receptor binding protein; signal transduction;  
KW LDL receptor binding protein; LDL receptor signalling pathway.  
OS Synthetic.  
XX PN WO200184159-A2.  
XX PD 08-NOV-2001.  
XX PF 24-APR-2001; 2001WO-US013214.  
XX PR 01-MAY-2000; 2000US-00562737.  
XX

PA (TEXA ) UNIV TEXAS SYSTEM.  
XX Herz J, Gotthardt M;  
XX WPI; 2002-082855/11.  
DR  
XX  
XX Detecting stress that alters interaction of LDL receptor binding  
PT polypeptide with LDL receptor interaction domain, comprises detecting  
PT difference in stress-biased and unbiased interaction of peptide and  
PT domain in a system.  
XX  
XX Disclosure; Page 148-150; 200pp; English.  
XX  
CC The present invention describes a method for detecting a stress that  
CC alters a functional interaction of a low density lipoprotein (LDL)  
CC receptor binding protein (I) with an LDL receptor interaction domain  
CC (II). The method involves introducing a predetermined stress into a  
CC system which provides a stress-biased physical interaction of (I) with  
CC (II), where in the absence of the stress, the system provides an unbiased  
CC interaction of (I) and (II), and detecting the stress-biased interaction  
CC of (I) and (II), where a difference between BI and UI indicates that the  
CC stress alters the interaction of (I) and (II). (I) is selected from  
CC SEMCAP-1, JIP-1, PSD-95, JIP-2, Talin, OMP25, CAPON, PIP4,5 Kinase, Na  
CC channel brain 3, Mint1, ICAP-1 and APC subunit 10. The method is useful  
CC for detecting a stress that alters functional interaction of LDL receptor  
CC binding polypeptide with LDL receptor interaction domain. The method is  
CC useful for detecting and modulating signal transduction through LDL  
CC receptors. ABB04778 to ABB04909 represent LDL receptor binding proteins  
CC which are used in the exemplification of the present invention  
XX  
SQ Sequence 1024 AA;  
  
Query Match 61.8%; Score 44.5; DB 5; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 6.5e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 CGYWL-TIWGC 10  
|||:|:|  
Db 892 CGHWIETMWD 902  
  
RESULT 13  
ADP29850  
ID ADP29850 standard; protein; 149 AA.  
XX  
AC ADP29850;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #617.  
XX  
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
XX Homo sapiens.  
OS  
XX WO2004035732-A2.  
PN  
XX  
PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
XX 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.

PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
XX Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
DR  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 1848; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule



CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOWEB and is not in the specification.

XX  
SQ Sequence 149 AA;

Query Match 61.1%; Score 44; DB 8; Length 149;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
| :|||:|  
Db 95 CHFWLTWV 102

RESULT 14  
AAE31487  
ID AAE31487 standard; protein; 166 AA.  
XX  
AC AAE31487;  
XX  
DT 24-FEB-2003 (first entry)  
DE Human butryophilin 2/3 protein.  
XX  
KW Human; B7-H1.2 protein; Butryophilin 2/3 protein; transplant rejection;  
KW immunological condition; graft-versus-host disease; allergy; asthma;  
KW inflammatory bowel disease; sepsis; Alzheimer's disease; atherosclerosis;  
KW T-cell mediated inflammation; autoimmune disease; multiple sclerosis;  
KW systemic lupus erythematosus; autoimmune demyelination; Grave's disease;  
KW psoriasis; autoimmune diabetes; diabetic neuropathy; HIV infection;  
KW rheumatoid arthritis; human immunodeficiency virus; immunosuppressive;  
KW gene therapy; infection; virucide.

XX  
OS Homo sapiens.  
XX  
PN WO200279474-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 08-JAN-2002; 2002WO-US000590.  
XX  
PR 08-JAN-2001; 2001US-0260617P.  
PR 19-JAN-2001; 2001US-0262737P.  
PR 07-JAN-2002; 2002US-00260617.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Baum PR, Dubose RF, Wiley SR;  
XX  
DR WPI; 2003-046816/04.  
XX  
PT New B7-H1.2 or Butryophilin 2/3 polypeptide of the human B7 polypeptide  
PT family, useful for treating an immunological condition e.g. transplant  
PT rejection.

XX  
PS Example 1; Page 64-65; 99pp; English.

XX  
CC The invention relates to B7-H1.2 or Butryophilin 2/3 polypeptides of  
CC human B7 polypeptide family and polynucleotides encoding such proteins.  
CC Sequences of the invention are useful for treating an immunological  
CC conditions (e.g., transplant rejection, graft-versus-host disease,  
CC allergy, asthma, inflammatory bowel disease, sepsis), diseases that are  
CC caused or exacerbated by T-cell mediated inflammation (e.g., Alzheimer's  
CC disease or atherosclerosis), autoimmune diseases (e.g., systemic lupus  
CC erythematosus, autoimmune demyelination, Grave's disease, psoriasis,  
CC multiple sclerosis, autoimmune diabetes, diabetic neuropathy, rheumatoid  
CC arthritis), bacterial or viral infections such as human immunodeficiency  
CC virus (HIV) infection, delayed reconstitution of T-cells, defects in T-

CC cell or accessory cell function or congenital immunodeficiencies. They  
CC are also used in gene therapy. The present sequence is human butryophilin  
CC consensus protein

XX  
SQ Sequence 166 AA;

Query Match 61.1%; Score 44; DB 6; Length 166;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTIWGC 10  
|| :|||  
Db 127 YWEVWGC 134

RESULT 15  
AAU91293  
ID AAU91293 standard; protein; 415 AA.  
XX  
AC AAU91293;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human NOV8 protein.  
XX  
KW Human; NOVX; gene therapy; cardiomyopathy; atherosclerosis; diabetes;  
KW cell signal processing; metabolic pathway modulation; inflammation;  
KW autoimmune disorder; scleroderma; transplantation; allergy;  
KW systemic lupus erythematosus; haemophilia; Alzheimer's disease;  
KW graft versus host disease; Lesch-Nyhan syndrome; periodontitis;  
KW pancreatitis; musculoskeletal disorder; Parkinson's disease;  
KW Huntington's disease; behavioural disorder; pain; obesity; wound healing;  
KW neurodegenerative disorder; neuropsychiatric disorder; hypertension;  
KW growth disorder; reproductive disorder; lung disease.

XX  
OS Homo sapiens.  
XX  
PN WO200216600-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026518.  
XX  
PR 25-AUG-2000; 2000US-0227800P.  
PR 25-AUG-2000; 2000US-0228205P.  
PR 25-AUG-2000; 2000US-0228324P.  
PR 30-AUG-2000; 2000US-0228997P.  
PR 30-AUG-2000; 2000US-0229185P.  
PR 01-SEP-2000; 2000US-0229780P.  
PR 01-SEP-2000; 2000US-0229848P.  
PR 01-SEP-2000; 2000US-0229850P.  
PR 22-JAN-2001; 2001US-0263337P.  
PR 31-JAN-2001; 2001US-0265518P.  
PR 15-MAR-2001; 2001US-0276451P.  
PR 27-MAR-2001; 2001US-0279196P.  
PR 24-AUG-2001; 2001US-00939398.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Gerlach V, Macdougall JR, Smithson G, Stone DJ, Ellerman K;  
PI Spytek KA, Zerhusen BD, Rastelli L, Verney CAM, Patturajan M;  
PI Tchernev VT, Padigaru M, Taupier RJ;  
XX  
DR WPI; 2002-292064/33.  
DR N-PSDB; ABK55577.  
XX  
PT New isolated cytoplasmic, nuclear, membrane bound and secreted  
PT polypeptides, termed NOVX, useful for treating inflammation, autoimmune  
PT disorders, hemophilia, Lesch-Nyhan syndrome, pancreatitis,  
PT musculoskeletal disorders.

XX  
PS Claim 1; Page 108; 245pp; English.



CC The invention relates to an isolated cytoplasmic, nuclear, membrane bound  
CC or secreted polypeptide, designated NOVX (actually NOV1, 2a, 2b, 3a, 3b,  
CC 4, 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, a  
CC mature form, or a variant of the mature form of NOVX. Also included are a  
CC polynucleotide encoding NOVX (or its complement), a vector comprising the  
CC polynucleotide, a cell comprising the vector, an anti-NOVX antibody,  
CC determining the presence of NOVX in a sample using the antibody,  
CC which binds to NOVX polynucleotide, identifying a agent which binds to  
CC NOVX (including modulators of NOVX). NOVX, the polynucleotide and the  
CC antibody are useful for diagnosing, treating or preventing a NOVX-  
CC associated disorder selected from cardiomyopathy, atherosclerosis,  
CC diabetes, a disorder related to cell signal processing and metabolic  
CC pathway modulation, inflammation, autoimmune disorders, scleroderma,  
CC transplantaton, allergies, systemic lupus erythematosus, haemophilia,  
CC graft versus host disease, Alzheimer's disease, stroke, Lesch-Nyhan  
CC syndrome, periodontitis, pancreatitis, musculoskeletal disorders,  
CC Parkinson's disease, Huntington's disease, behavioural disorders, pain,  
CC neurodegenerative and neuropsychiatric disorders, hypertension, wound  
CC healing, obesity, growth and reproductive disorders, lung diseases and  
CC many other diseases and disorders listed in the specification. NOVX, the  
CC polynucleotide and the antibody are useful in screening assays, detection  
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),  
CC predictive medicine (e.g., diagnostic assays, prognostic assays,  
CC monitoring clinical trials and pharmacogenomic), and in methods of  
CC treatment (e.g., therapeutic and prophylactic). NOVX is useful as  
CC immunogen to produce antibodies immunospecific for NOVX, as vaccines to  
CC screen for potential agonist and antagonist compounds, and as bait  
CC protein in a two-hybrid or three-hybrid assay. The polynucleotide is  
CC useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic  
CC lesion in a NOVX gene, and to modulate NOVX activity. The vector is  
CC useful for producing non-human transgenic animals. The antibody is useful  
CC for isolating, and purifying NOVX and to monitor protein levels in tissue  
CC as part of a clinical testing procedure. The present sequence represents  
CC a NOVX protein

XX

SQ Sequence 415 AA;

Query Match 61.1%; Score 44; DB 5; Length 415;  
Best Local Similarity 62.5%; Pred. No. 3.5e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGYWLTIW 8  
| :|||:|  
Db 95 CHEWLTW 102

Search completed: December 30, 2004, 13:07:53  
Job time : 72.6226 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 23.0189 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44.5	61.8	1024	4 US-09-562-737-84	Sequence 84, Appl
2	43	59.7	492	4 US-09-107-532A-6945	Sequence 6945, Ap
3	42.5	59.0	1024	4 US-09-562-737-86	Sequence 86, Appl
4	42.5	59.0	1765	4 US-09-354-147C-2	Sequence 2, Appli
5	42.5	59.0	1765	4 US-09-354-147C-3	Sequence 3, Appli
6	42	58.3	161	4 US-09-325-932A-187	Sequence 187, App
7	42	58.3	273	4 US-09-270-767-46926	Sequence 46926, A
8	42	58.3	1498	4 US-09-792-616-9	Sequence 9, Appli
9	42	58.3	1503	4 US-09-792-616-3	Sequence 3, Appli
10	41	56.9	222	4 US-09-071-035-408	Sequence 408, App
11	41	56.9	229	4 US-09-134-000C-3630	Sequence 3630, Ap
12	41	56.9	264	4 US-09-540-236-2978	Sequence 2978, Ap
13	41	56.9	266	4 US-09-071-035-406	Sequence 406, App
14	40.5	56.2	1024	4 US-09-562-737-81	Sequence 81, Appl
15	40.5	56.2	1024	4 US-09-562-737-87	Sequence 87, Appl
16	40.5	56.2	1835	3 US-08-836-325-15	Sequence 15, Appl
17	40.5	56.2	1835	4 US-09-457-571-15	Sequence 15, Appl
18	40.5	56.2	1836	4 US-10-162-012-24	Sequence 24, Appl
19	40.5	56.2	1969	3 US-08-836-325-16	Sequence 16, Appl
20	40.5	56.2	1969	4 US-09-457-571-16	Sequence 16, Appl
21	40.5	56.2	1976	3 US-09-024-020B-9	Sequence 9, Appli
22	40.5	56.2	1976	3 US-09-425-043-9	Sequence 9, Appli
23	40.5	56.2	1977	4 US-09-976-594-757	Sequence 757, App
24	40.5	56.2	1977	4 US-09-919-039-367	Sequence 367, App
25	40.5	56.2	1978	3 US-09-024-020B-3	Sequence 3, Appli
26	40.5	56.2	1978	3 US-09-425-043-3	Sequence 3, Appli
27	40.5	56.2	1984	3 US-08-836-325-10	Sequence 10, Appl

28	40.5	56.2	1984	4 US-09-457-571-10	Sequence 10, Appl
29	40.5	56.2	1988	3 US-09-024-020B-4	Sequence 4, Appli
30	40.5	56.2	1988	3 US-09-425-043-4	Sequence 4, Appli
31	40.5	56.2	1989	3 US-08-836-325-11	Sequence 11, Appl
32	40.5	56.2	1989	3 US-08-836-325-12	Sequence 12, Appl
33	40.5	56.2	1989	4 US-09-457-571-11	Sequence 11, Appl
34	40.5	56.2	1989	4 US-09-457-571-12	Sequence 12, Appl
35	40.5	56.2	2005	3 US-08-836-325-7	Sequence 7, Appli
36	40.5	56.2	2005	4 US-09-457-571-7	Sequence 7, Appli
37	40.5	56.2	2016	3 US-09-634-920-4	Sequence 4, Appli
38	40.5	56.2	2016	4 US-09-514-907A-2	Sequence 2, Appli
39	40.5	56.2	2016	4 US-09-896-994-2	Sequence 2, Appli
40	40.5	56.2	2016	4 US-09-840-125-4	Sequence 4, Appli
41	40	55.6	362	1 US-08-415-751-6	Sequence 6, Appli
42	40	55.6	668	4 US-09-248-796A-19350	Sequence 19350, A
43	39.5	54.9	73	4 US-09-513-999C-4541	Sequence 4541, Ap
44	39	54.2	430	4 US-09-443-041A-18	Sequence 18, Appl
45	39	54.2	450	4 US-09-443-041A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-09-562-737-84  
; Sequence 84, Application US/09562737  
; Patent No. 6428967  
; GENERAL INFORMATION:  
; APPLICANT: Herz, Joachim  
; APPLICANT: Gotthardt, Michael  
; TITLE OF INVENTION: LDL Receptor Signaling Pathways  
; FILE REFERENCE: UTSW0708  
; CURRENT APPLICATION NUMBER: US/09/562,737  
; CURRENT FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 84  
; LENGTH: 1024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-84

Query Match 61.8%; Score 44.5; DB 4; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
||:|:|:|  
Db 892 CGHWIETMDC 902

RESULT 2

US-09-107-532A-6945  
; Sequence 6945, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC

;  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6945:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 492 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...492  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6945:  
US-09-107-532A-6945

Query Match 59.7%; Score 43; DB 4; Length 492;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
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Db 112 GYWLTCW 118

RESULT 3  
US-09-562-737-86  
; Sequence 86, Application US/09562737  
; Patent No. 6428967  
; GENERAL INFORMATION:  
; APPLICANT: Herz, Joachim  
; APPLICANT: Gotthardt, Michael  
; TITLE OF INVENTION: LDL Receptor Signaling Pathways  
; FILE REFERENCE: UTSW0708  
; CURRENT APPLICATION NUMBER: US/09/562,737  
; CURRENT FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 86  
; LENGTH: 1024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-86

Query Match 59.0%; Score 42.5; DB 4; Length 1024;  
Best Local Similarity 63.6%; Pred. No. 3.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||  
Db 892 CGEWLETMWDC 902

RESULT 4

US-09-354-147C-2  
; Sequence 2, Application US/09354147C  
; Patent No. 6573067  
; GENERAL INFORMATION:  
; APPLICANT: Dib-Hajj, Sulayman  
; APPLICANT: Waxman, Stephen G.  
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
; FILE REFERENCE: 44574-5004-01-US  
; CURRENT APPLICATION NUMBER: US/09/354,147C  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US 60/072,990  
; PRIOR FILING DATE: 1998-01-29  
; PRIOR APPLICATION NUMBER: US 60/109,402  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: PCT/US99/02008  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (652)..(1334)  
; OTHER INFORMATION: Xaa at position 652 is Leu; Xaa at position 1334 is Asn  
; OTHER INFORMATION: or Lys. Xaa's result from n's in SEQ ID NO: 1.  
US-09-354-147C-2

Query Match 59.0%; Score 42.5; DB 4; Length 1765;  
Best Local Similarity 54.5%; Pred. No. 5.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||  
Db 754 CGEWIENMWGC 764

RESULT 5  
US-09-354-147C-3  
; Sequence 3, Application US/09354147C  
; Patent No. 6573067  
; GENERAL INFORMATION:  
; APPLICANT: Dib-Hajj, Sulayman  
; APPLICANT: Waxman, Stephen G.  
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
; FILE REFERENCE: 44574-5004-01-US  
; CURRENT APPLICATION NUMBER: US/09/354,147C  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US 60/072,990  
; PRIOR FILING DATE: 1998-01-29  
; PRIOR APPLICATION NUMBER: US 60/109,402  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: PCT/US99/02008  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: putative amino acid seq. of rat Nan  
US-09-354-147C-3

Query Match 59.0%; Score 42.5; DB 4; Length 1765;  
Best Local Similarity 54.5%; Pred. No. 5.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||  
Db 754 CGEWIENMWGC 764

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RESULT 6
US-09-325-932A-187
; Sequence 187, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-187

Query Match      58.3%; Score 42; DB 4; Length 161;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIWC 10
      |||||: ||
Db      100 GYWLNLGSC 108

RESULT 7
US-09-270-767-46926
; Sequence 46926, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46926
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46926

Query Match      58.3%; Score 42; DB 4; Length 273;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWLTIW 8
      |||||: ||
Db      266 CGYWATIF 273

RESULT 8
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match      58.3%; Score 42; DB 4; Length 1498;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||||: |
Db      960 GYWLSLW 966

RESULT 9
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      58.3%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||||: |
Db      965 GYWLSLW 971

RESULT 10
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
```



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 408:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 222 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-071-035-408

Query Match 56.9%; Score 41; DB 4; Length 222;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | : | : |  
Db 179 GTWITLWG 186

RESULT 11  
US-09-134-000C-3630  
Sequence 3630, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3630  
LENGTH: 229  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-3630

Query Match 56.9%; Score 41; DB 4; Length 229;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | : | : |  
Db 203 GTWITLWG 210

RESULT 12  
US-09-540-236-2978  
Sequence 2978, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2005-001  
CURRENT APPLICATION NUMBER: US/09/540,236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 2978  
LENGTH: 264  
TYPE: PRT  
ORGANISM: M.catarrhalis  
US-09-540-236-2978

Query Match 56.9%; Score 41; DB 4; Length 264;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
| | : | : |  
Db 200 CGAWLGIW 207

RESULT 13  
US-09-071-035-406  
Sequence 406, Application US/09071035  
Patent No. 6448043  
GENERAL INFORMATION:  
APPLICANT: Gil H. Choi  
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 496  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,035  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: A. Anders Brookes  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB369P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 406:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-071-035-406

Query Match 56.9%; Score 41; DB 4; Length 266;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | : | : |  
Db 203 GTWITLWG 210

RESULT 14  
US-09-562-737-81  
Sequence 81, Application US/09562737  
Patent No. 6428967  
GENERAL INFORMATION:  
APPLICANT: Herz, Joachim  
APPLICANT: Gotthardt, Michael  
TITLE OF INVENTION: LDL Receptor Signaling Pathways  
FILE REFERENCE: UTSW0708  
CURRENT APPLICATION NUMBER: US/09/562,737  
CURRENT FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 81  
LENGTH: 1024  
TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-81

Query Match 56.2%; Score 40.5; DB 4; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 5.8e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||:|:|  
Db 892 CGEWIGTMWDC 902

RESULT 15  
US-09-562-737-87  
; Sequence 87, Application US/09562737  
; Patent No. 6428967  
; GENERAL INFORMATION:  
; APPLICANT: Herz, Joachim  
; APPLICANT: Gotthardt, Michael  
; TITLE OF INVENTION: LDL Receptor Signaling Pathways  
; FILE REFERENCE: UTSW0708  
; CURRENT APPLICATION NUMBER: US/09/562,737  
; CURRENT FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 87  
; LENGTH: 1024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-87

Query Match 56.2%; Score 40.5; DB 4; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 5.8e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||:|:|  
Db 892 CGEWIGTMWDC 902

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(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGWLTWGC 10

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Gapop 10.0 , Gapext 0.5

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Listing first 45 summaries

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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	13	US-10-046-922-35
2	54	75.0	10	13	US-10-046-922-34
3	50	69.4	10	13	US-10-046-922-73
4	47.5	66.0	304	14	US-10-017-161-2288
5	47.5	66.0	304	14	US-10-292-798-1934
6	47	65.3	25	14	US-10-280-066-476
7	47	65.3	63	16	US-10-437-963-125253
8	46	63.9	17	14	US-10-125-869A-54
9	46	63.9	17	15	US-10-462-262-278
10	46	63.9	136	15	US-10-112-944-743
11	45	62.5	828	15	US-10-282-122A-77862
12	44.5	61.8	1024	14	US-10-211-962-84
13	44	61.1	103	16	US-10-437-963-181150

14	44	61.1	161	16	US-10-767-701-54778	Sequence 54778, A
15	43	59.7	13	14	US-10-125-869A-73	Sequence 73, Appl
16	43	59.7	13	15	US-10-462-262-297	Sequence 297, App
17	43	59.7	291	14	US-10-369-493-19313	Sequence 19313, A
18	43	59.7	454	14	US-10-032-585-7816	Sequence 7816, Ap
19	43	59.7	459	16	US-10-437-963-160191	Sequence 160191,
20	43	59.7	474	15	US-10-282-122A-57928	Sequence 57928, A
21	43	59.7	671	16	US-10-437-963-190740	Sequence 190740,
22	42.5	59.0	152	11	US-09-833-245-1533	Sequence 1533, Ap
23	42.5	59.0	152	15	US-10-264-237-2457	Sequence 2457, Ap
24	42.5	59.0	159	11	US-09-833-245-1534	Sequence 1534, Ap
25	42.5	59.0	161	15	US-10-276-774-2376	Sequence 2376, Ap
26	42.5	59.0	161	15	US-10-296-115-1337	Sequence 1337, Ap
27	42.5	59.0	176	14	US-10-161-927-10	Sequence 10, Appl
28	42.5	59.0	1024	14	US-10-211-962-86	Sequence 86, Appl
29	42.5	59.0	1765	14	US-10-388-470-2	Sequence 2, Appli
30	42.5	59.0	1765	14	US-10-388-470-3	Sequence 3, Appli
31	42	58.3	90	11	US-09-864-408A-8146	Sequence 8146, Ap
32	42	58.3	161	14	US-10-219-220-187	Sequence 187, App
33	42	58.3	1498	10	US-09-792-616-9	Sequence 9, Appli
34	42	58.3	1498	16	US-10-764-328-9	Sequence 9, Appli
35	42	58.3	1503	10	US-09-792-616-3	Sequence 3, Appli
36	42	58.3	1503	16	US-10-764-328-3	Sequence 3, Appli
37	41.5	57.6	122	15	US-10-108-260A-2641	Sequence 2641, Ap
38	41.5	57.6	620	14	US-10-369-493-119	Sequence 119, App
39	41	56.9	14	14	US-10-125-869A-114	Sequence 114, App
40	41	56.9	14	15	US-10-462-262-338	Sequence 338, App
41	41	56.9	34	9	US-09-864-761-43458	Sequence 43458, A
42	41	56.9	57	15	US-10-424-599-179308	Sequence 179308,
43	41	56.9	78	17	US-10-425-115-204642	Sequence 204642,
44	41	56.9	82	15	US-10-424-599-240891	Sequence 240891,
45	41	56.9	104	17	US-10-425-115-332065	Sequence 332065,

ALIGNMENTS

RESULT 1  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; TYPE: PRT  
; ORGANISM: isolated peptide  
US-10-046-922-35

Query Match 100.0%; Score 72; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGWLTWGC 10  
| | | | | | | | | |  
Db 1 CGWLTWGC 10

RESULT 2  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki

; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
; US-10-046-922-34

Query Match 75.0%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
Db 2 GYWLTIWG 9

RESULT 3
US-10-046-922-73
; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 10
; TYPE: PRT
; ORGANISM: peptide library
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(7)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: X is any amino acid
; US-10-046-922-73

Query Match 69.4%; Score 50; DB 13; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
Db 1 CGYWXXXWXC 10

RESULT 4
US-10-017-161-2288
; Sequence 2288, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA

; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2288
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (73)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (79)..(83)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (85)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (89)..(91)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (96)..(97)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (101)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (107)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (118)..(119)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (121)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (123)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (162)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (178)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (194)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (210)..(211)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD\_RES
; LOCATION: (219)
; OTHER INFORMATION: Variable amino acid



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;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-2288

Query Match      66.0%; Score 47.5; DB 14; Length 304;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY      1 CGYWLTIWGC 10
      ||:| :|||
Db      108 CGFW-AVWGC 116

RESULT 5
US-10-292-798-1934
; Sequence 1934, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1934
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (73)..(73)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (80)..(83)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (89)..(91)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (96)..(97)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (101)..(101)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (107)..(107)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (118)..(119)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (121)..(121)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (123)..(123)
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; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (178)..(178)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (210)..(211)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (219)..(219)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-292-798-1934

Query Match      66.0%; Score 47.5; DB 14; Length 304;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY      1 CGYWLTIWGC 10
      ||:| :|||
Db      108 CGFW-AVWGC 116

RESULT 6
US-10-280-066-476
; Sequence 476, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINDI
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 476
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Eschericia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Tiel-20C-3-D116
US-10-280-066-476

Query Match      65.3%; Score 47; DB 14; Length 25;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGYWLTIWG 9
      |||| :||
Db      5 CGYWGELWG 13

RESULT 7
US-10-437-963-125253
; Sequence 125253, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 125253
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27915C.1.pep
US-10-437-963-125253

Query Match      65.3%; Score 47; DB 16; Length 63;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
Db      37 CGHYLKAWGC 46

RESULT 8
US-10-125-869A-54
; Sequence 54, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-54

Query Match      63.9%; Score 46; DB 14; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGYWLTIWG 9
Db      4 CGFWPRIWG 12

RESULT 9
US-10-462-262-278
; Sequence 278, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
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; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-278

Query Match      63.9%; Score 46; DB 15; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGYWLTIWG 9
Db      4 CGFWPRIWG 12

RESULT 10
US-10-112-944-743
; Sequence 743, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 743
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(136)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for
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; OTHER INFORMATION: in Example 2
US-10-112-944-743
  Query Match      63.9%; Score 46; DB 15; Length 136;
  Best Local Similarity 60.0%; Pred. No. 73;
  Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
Db      93 CGRWDWLWGC 102

RESULT 11
US-10-282-122A-77862
; Sequence 77862, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77862
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-282-122A-77862
  Query Match      62.5%; Score 45; DB 15; Length 828;
  Best Local Similarity 58.3%; Pred. No. 4.3e+02;
  Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY      1 CGYWLTI--WGC 10
Db      372 CGLWLELLSWGC 383

RESULT 12
US-10-211-962-84
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; Sequence 84, Application US/10211962
; Publication No. US20030082640A1
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/10/211,962
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/562,737
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-10-211-962-84
  Query Match      61.8%; Score 44.5; DB 14; Length 1024;
  Best Local Similarity 54.5%; Pred. No. 6e+02;
  Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
Db      892 CGHWIETMWDC 902

RESULT 13
US-10-437-963-181150
; Sequence 181150, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 181150
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78451C.1.pep
US-10-437-963-181150
  Query Match      61.1%; Score 44; DB 16; Length 103;
  Best Local Similarity 50.0%; Pred. No. 1.1e+02;
  Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 YWLTIWGC 10
Db      19 WWVSVWGC 26

RESULT 14
US-10-767-701-54778
; Sequence 54778, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 54778
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14593586.pep
US-10-767-701-54778
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Query Match      61.1%; Score 44; DB 16; Length 161;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 CGYWLTIW 8
      |||||
Db      150 CGYWLKPW 157
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RESULT 15
US-10-125-869A-73
; Sequence 73, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-73
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Query Match      59.7%; Score 43; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      2 GYWLTIWG 9
      |||:|
Db      1 GYWCNVWG 8
```

Search completed: December 30, 2004, 13:50:01  
Job time : 75.5283 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	63.9	218	2 S76385	hypothetical prote
2	45	62.5	828	2 AD0412	ATP-dependent heli
3	43.5	60.4	1993	2 T30902	sodium channel sca
4	42.5	59.0	1765	2 T42388	sodium channel alp
5	42	58.3	72	2 S30980	gene 35 protein -
6	42	58.3	441	2 C95307	probable transport
7	42	58.3	1502	2 T42216	multidrug resistan
8	41.5	57.6	620	2 F70439	oxaloacetate decar
9	41	56.9	307	2 T48166	hypothetical prote
10	41	56.9	391	2 PC4117	replication protei
11	41	56.9	419	2 E90446	permease imported
12	41	56.9	739	2 T29407	hypothetical prote
13	40.5	56.2	200	2 I48108	sodium channel alp
14	40.5	56.2	1681	2 A55138	sodium channel mNa
15	40.5	56.2	1682	2 A45380	sodium channel pro
16	40.5	56.2	1820	1 CHEE	sodium channel pro
17	40.5	56.2	1835	2 I54323	sodium channel alp
18	40.5	56.2	1836	2 I64893	sodium channel alp
19	40.5	56.2	1836	2 JS0648	sodium channel alp
20	40.5	56.2	1836	2 I51964	sodium channel alp
21	40.5	56.2	1840	1 CHRTM1	sodium channel pro
22	40.5	56.2	1951	2 S00320	sodium channel pro
23	40.5	56.2	1976	2 I56555	sodium channel pro
24	40.5	56.2	1977	2 S54771	sodium channel alp
25	40.5	56.2	1983	2 A60054	sodium channel pro
26	40.5	56.2	2005	2 A46269	sodium channel alp
27	40.5	56.2	2005	2 B25019	sodium channel pro
28	40.5	56.2	2009	2 A25019	sodium channel pro
29	40.5	56.2	2016	2 A38195	sodium channel pro

30	40.5	56.2	2019	2 A33996	sodium channel pro
31	40.5	56.2	2049	2 T43161	sodium channel pro
32	40	55.6	142	2 C34903	Ig heavy chain pre
33	40	55.6	339	2 F97190	phenylalanyl-tRNA
34	40	55.6	359	2 F95406	probable ABC trans
35	40	55.6	425	2 B71038	probable Na+/H+-ex
36	40	55.6	508	2 C95282	probable ABC trans
37	40	55.6	2344	2 S64740	genome polyprotein
38	39.5	54.9	298	2 AH0289	probable aldo/keto
39	39.5	54.9	345	1 JH0185	D-amino-acid oxida
40	39.5	54.9	347	1 OXPGDA	D-amino-acid oxida
41	39.5	54.9	347	1 S01340	D-amino-acid oxida
42	39.5	54.9	347	1 JX0132	D-amino-acid oxida
43	39	54.2	376	2 AF1978	hypothetical prote
44	39	54.2	392	2 A53580	neurexin III beta
45	39	54.2	426	2 B53580	neurexin III beta

ALIGNMENTS

RESULT 1

S76385  
hypothetical protein - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.

A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S76385

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis 6803.

A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S76385  
A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-218 <KAN>

A;Cross-references: UNIPROT:Q55705; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA1023;  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: probable alkaline phosphatase yngC

Query Match 63.9%; Score 46; DB 2; Length 218;  
Best Local Similarity 66.7%; Pred. No. 8.1;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWG 9

Db 73 CGYWVGRWG 81

RESULT 2

AD0412

ATP-dependent helicase [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AD0412

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Eil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, H.; Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AD0412

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-828 <KUR>

A;Cross-references: UNIPROT:Q8ZBL4; GB:AL590842; PIDN:CAC92624.1; PID:g15981320; GSPDB:G

C;Genetics:

A;Gene: hrpB

C;Superfamily: ATP-dependent RNA helicase, HrpB type

Query Match 62.5%; Score 45; DB 2; Length 828;



Best Local Similarity 58.3%; Pred. No. 36;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
  
QY 1 CGYWLTI--WGC 10  
||| | : |||  
Db 372 CGLWLELLSWGC 383  
  
RESULT 3  
T30902 sodium channel SCAP1 alpha chain - California sea hare  
C;Species: Aplysia californica (California sea hare)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30902  
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.  
DNA Cell Biol. 16, 347-356, 1997  
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.  
A;Reference number: Z20929; MUID:97238630; PMID:9115644  
A;Accession: T30902  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1993 <DYE>  
A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474  
C;Superfamily: sodium channel protein  
  
Query Match 60.4%; Score 43.5; DB 2; Length 1993;  
Best Local Similarity 54.5%; Pred. No. 1.3e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 CGYWL-TIWGC 10  
|| | : : |||  
Db 942 CGEWIESMWGC 952  
  
RESULT 4  
T42388 sodium channel alpha chain - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T42388  
R;Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.  
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998  
A;Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in peripheral  
A;Reference number: Z22149; MUID:98338024; PMID:9671787  
A;Accession: T42388  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1765 <DIB>  
A;Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4  
A;Experimental source: strain Sprague-Dawley; dorsal root ganglia  
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trigem  
C;Superfamily: sodium channel protein  
  
Query Match 59.0%; Score 42.5; DB 2; Length 1765;  
Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
  
QY 1 CGYWL-TIWGC 10  
|| | : : |||  
Db 754 CGEWIENMWGC 764  
  
RESULT 5  
S30980 gene 35 protein - Mycobacterium phage L5  
C;Species: Mycobacterium phage L5  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: S30980  
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.  
Mol. Microbiol. 7, 407-417, 1993  
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans  
A;Reference number: S30949; MUID:93211283; PMID:8459767  
A;Accession: S30980

A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-72 <DON>  
A;Cross-references: UNIPROT:Q05245; EMBL:Z18946; NID:g15859; PIDN:CAA79411.1; PID:g15891  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
C;Genetics:  
A;Gene: 35  
  
Query Match 58.3%; Score 42; DB 2; Length 72;  
Best Local Similarity 62.5%; Pred. No. 12;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 CGYWLTIW 8  
||| | : |  
Db 50 CGMWLPVW 57  
  
RESULT 6  
C95307 probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) mag  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: C95307  
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A;Reference number: A95262; MUID:21396509; PMID:11481432  
A;Accession: C95307  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-441 <KUR>  
A;Cross-references: UNIPROT:Q92ZT6; GB:AB006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:GN  
A;Experimental source: strain 1021, megaplasmid pSyma  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
heault, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: Sma0684  
A;Genome: plasmid  
C;Superfamily: L-lysine transport protein  
  
Query Match 58.3%; Score 42; DB 2; Length 441;  
Best Local Similarity 71.4%; Pred. No. 58;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GYWLTIW 8  
||| : |||  
Db 92 GYWISIW 98  
  
RESULT 7  
T42216 multidrug resistance-associated protein homolog MLP-1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T42216  
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.  
Mol. Pharmacol. 53, 1068-1075, 1998  
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins main  
A;Reference number: Z22081; MUID:98279126; PMID:9614210  
A;Accession: T42216  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1502 <HIR>  
A;Cross-references: UNIPROT:O88269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g32  
A;Experimental source: strain Sprague-Dawley; liver

C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 58.3%; Score 42; DB 2; Length 1502;  
Best Local Similarity 71.4%; Pred. NO. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||:|

Db 964 GYWLSLW 970

RESULT 8  
F70439  
oxaloacetate decarboxylase alpha chain - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: F70439  
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
V.

Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: F70439  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-620 <AQF>  
A;Cross-references: UNIPROT:O67544; GB:AE000747; NID:g2983944; PIDN:AAC07497.1; PID:g298  
A;Experimental source: strain VFS  
C;Genetics:  
A;Gene: oadA

C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio  
F;540-613/Domain: lipoyl/biotin-binding homology <LPB>  
F;579/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 57.6%; Score 41.5; DB 2; Length 620;  
Best Local Similarity 60.0%; Pred. NO. 93;  
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYW-LTIWG 9  
|||:|

Db 38 CGFWSLEWVG 47

RESULT 9  
T48166  
hypothetical protein T1008.150 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48166  
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: 224486  
A;Accession: T48166  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-307 <BEV>  
A;Cross-references: UNIPROT:Q9M030; EMBL:AL161746  
A;Experimental source: cultivar Columbia; BAC clone T1008  
C;Genetics:  
A;Map position: 5  
A;Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1  
A;Note: T1008.150

Query Match 56.9%; Score 41; DB 2; Length 307;  
Best Local Similarity 50.0%; Pred. NO. 60;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
|:|:|

Db 186 CSFWSIWGC 195

RESULT 10

PC4117  
replication protein homolog - Pyrococcus sp. (fragment)  
N;Alternate names: hypothetical 391 protein  
C;Species: Pyrococcus sp.  
C;Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 17-May-1996  
C;Accession: PC4117  
R;Rashid, N.; Morikawa, M.; Imanaka, T.  
Gene 166, 139-143, 1995  
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.  
A;Reference number: JC4514; MUID:96105215; PMID:8529878  
A;Accession: PC4117  
A;Molecule type: DNA  
A;Residues: 1-391 <RAS>  
A;Cross-references: DDBJ:D50018

Query Match 56.9%; Score 41; DB 2; Length 391;  
Best Local Similarity 85.7%; Pred. NO. 74;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YWLTIWG 9  
|||:|

Db 155 YWLTEWG 161

RESULT 11  
E90446  
permease [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: E90446  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: E90446  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-419 <KUR>  
A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G  
C;Genetics:  
A;Gene: SSO2718

Query Match 56.9%; Score 41; DB 2; Length 419;  
Best Local Similarity 62.5%; Pred. NO. 78;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
|||:|

Db 365 GFWETLWG 372

RESULT 12  
T29407  
hypothetical protein C16C8.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C;Accession: T29407  
R;Waterston, R.; Le, T.T.; Gattung, S.  
submitted to the EMBL Data Library, November 1996  
A;Description: The sequence of C. elegans cosmid C16C8.  
A;Reference number: Z20617  
A;Accession: T29407  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-739 <WAT>  
A;Cross-references: EMBL:U80452; PIDN:AAB37863.1; GSPDB:GN00020; CESP:C16C8.2  
A;Experimental source: strain Bristol N2; clone C16C8  
C;Genetics:  
A;Gene: CESP:C16C8.2  
A;Map position: 2  
A;Introns: 68/2; 179/3; 253/1; 275/3; 327/2; 365/3; 397/1; 428/2; 463/3; 629/1; 668/2; 72

C;Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 56.9%; Score 41; DB 2; Length 739;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10  
||:|||||  
Db 118 CGFWATIREC 127

RESULT 13

I48108  
sodium channel alpha subunit - long-tailed hamster (fragment)  
C;Species: Cricetulus longicaudatus (long-tailed hamster)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48108  
R;Lalalik, P.H.; Krafte, D.S.; Cicccarelli, R.B.  
Am. J. Physiol. 264, 803-809, 1993  
A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster  
A;Reference number: I48107  
A;Accession: I48108  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 1-200 <RES>  
A;Cross-references: UNIPROT:Q60464; GB:M87541; NID:g191069; PIDN:AAA36979.1; PID:g553840  
C;Genetics:  
A;Gene: cho1  
C;Superfamily: sodium channel protein  
C;Keywords: duplication

Query Match 56.2%; Score 40.5; DB 2; Length 200;  
Best Local Similarity 54.5%; Pred. No. 49;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||:|:|  
Db 26 CGEWIETLWDC 36

RESULT 14

A55138  
sodium channel mNa2.3, voltage-gated - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A55138  
R;Felipe, A.; Knittle, T.J.; Doyle, K.L.; Tamkun, M.M.  
J. Biol. Chem. 269, 30125-30131, 1994  
A;Title: Primary structure and differential expression during development and pregnancy  
A;Reference number: A55138; MUID:95074002; PMID:7982916  
A;Accession: A55138  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1681 <FEL>  
A;Cross-references: UNIPROT:Q62467; GB:L36179; NID:g609544; PIDN:AAA66192.1; PID:g806397  
C;Superfamily: sodium channel protein

Query Match 56.2%; Score 40.5; DB 2; Length 1681;  
Best Local Similarity 54.5%; Pred. No. 3.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||:|:|  
Db 686 CGEWIETLWEC 696

RESULT 15

A45380  
sodium channel protein alpha chain hNav2.1 - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: A45380  
R;George Jr., A.L.; Knittle, T.J.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992

A;Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in human  
A;Reference number: A45380; MUID:92279233; PMID:1317577  
A;Accession: A45380  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1682 <GEO>  
A;Cross-references: UNIPROT:Q01118; GB:M91556; NID:g189046; PIDN:AAA59899.1; PID:g189047  
A;Experimental source: heart  
A;Note: sequence extracted from NCBI backbone (NCBIP:104344)  
C;Superfamily: sodium channel protein  
C;Keywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-gated

Query Match 56.2%; Score 40.5; DB 2; Length 1682;  
Best Local Similarity 54.5%; Pred. No. 3.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10  
|||:|:|  
Db 686 CGEWIETLWDC 696

Search completed: December 30, 2004, 13:17:13  
Job time : 12.6761 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	63.9	218	1 Y232 SYN3	Q55705 synechocyst
2	45	62.5	828	2 Q8ZBL4	Q8zbl4 yersinia pe
3	45	62.5	853	2 Q8D1A7	Q8dla7 yersinia pe
4	45	62.5	853	2 AAS60566	Aas60566 yersinia
5	43.5	60.4	1993	2 P90670	P90670 aplysia cal
6	43	59.7	168	2 Q6H022	Q6h022 fremyella d
7	43	59.7	221	2 Q74JK6	Q74jk6 lactobacill
8	43	59.7	221	2 AAS08923	Aas08923 lactobaci
9	43	59.7	501	2 Q6C574	Q6c574 yarrowia li
10	43	59.7	646	2 Q8DKD6	Q8dkd6 synechococc
11	43	59.7	733	2 Q8H2N7	Q8h2n7 oryza sativ
12	43	59.7	1084	2 Q7WY20	Q7wy20 pseudomonas
13	42.5	59.0	152	2 Q96AC0	Q96ac0 homo sapien
14	42.5	59.0	159	2 Q6RW13	Q6rw13 homo sapien
15	42.5	59.0	159	2 Q9NRW9	Q9nrw9 homo sapien
16	42.5	59.0	159	2 Q96PL4	Q96pl4 homo sapien
17	42.5	59.0	159	2 AAR25556	Aar25556 homo sapi
18	42.5	59.0	263	2 Q7YYF1	Q7yyf1 cryptospori
19	42.5	59.0	1765	2 Q88457	Q88457 rattus norv
20	42	58.3	72	1 VC35 BPML5	Q05245 mycobacteri
21	42	58.3	133	2 Q855L3	Q855l3 mycobacteri
22	42	58.3	284	2 Q6MC01	Q6mc01 parachlamyd
23	42	58.3	284	2 CAF23898	Caf23898 parachlam
24	42	58.3	343	2 Q94FS2	Q94fs2 cajanus caj
25	42	58.3	389	2 Q83I51	Q83i51 tropheryma
26	42	58.3	441	2 Q92ZT6	Q92zt6 rhizobium m
27	42	58.3	452	2 Q83G14	Q83g14 tropheryma
28	42	58.3	472	1 RBL NITVU	Q596l3 nitrobacter
29	42	58.3	473	2 Q9XD76	Q9xd76 nitrobacter
30	42	58.3	473	2 Q9XD77	Q9xd77 nitrobacter
31	42	58.3	473	2 Q8VQ84	Q8vq84 nitrosospir

32	42	58.3	1308	2 Q8T6H2	Q8t6h2 dictyosteli
33	42	58.3	1498	1 MRP6 MOUSE	Q9rls7 mus musculu
34	42	58.3	1502	1 MRP6_RAT	O88269 rattus norv
35	42	58.3	1503	1 MRP6_HUMAN	O95255 homo sapien
36	41.5	57.6	122	2 Q8N1Z5	Q8n1z5 homo sapien
37	41.5	57.6	620	2 O67544	O67544 aquifex aeo
38	41	56.9	266	2 Q82285	Q82z85 enterococcu
39	41	56.9	307	2 Q9M030	Q9m030 arabidopsis
40	41	56.9	376	2 Q6CBE4	Q6cbe4 yarrowia li
41	41	56.9	398	2 Q8IUD8	Q8iud8 homo sapien
42	41	56.9	413	2 Q9HKA9	Q9hka9 thermoplasma
43	41	56.9	419	2 Q97VB7	Q97vb7 sulfolobus
44	41	56.9	432	2 Q6NUR0	Q6nur0 homo sapien
45	41	56.9	432	2 AAH59368	Aah59368 homo sapi

ALIGNMENTS

RESULT 1  
Y232\_SYN3  
ID Y232 SYN3 STANDARD; PRT; 218 AA.  
AC Q55705;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Hypothetical protein slr0232.  
GN OrderedLocusNames=slr0232;  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96127529; PubMed=8590279;  
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
RA Sugiyura M., Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
RT region from map positions 64% to 92% of the genome.";  
RL DNA Res. 2:153-166(1995).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to the deda family.

-----  
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DR EMBL; D64000; BAA10237.1; -.  
DR PIR; S76385; S76385.  
DR InterPro; IPR000252; Deda.  
DR Pfam; PF00597; Deda; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 218 AA; 23781 MW; C04B5D7B7EA7F863 CRC64;

Query Match 63.9%; Score 46; DB 1; Length 218;  
Best Local Similarity 66.7%; Pred. No. 50;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWG 9  
|||: ||  
Db 73 CGYWVGWRG 81

RESULT 2  
Q8ZBL4  
ID Q8ZBL4 PRELIMINARY; PRT; 828 AA.  
AC Q8ZBL4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)



DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ATP-dependent helicase.  
GN Name=hrpB; OrderedLocusNames=YPO3394;  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CO-92 / Biovar Orientalis;  
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;  
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,  
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,  
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,  
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
RT "Genome sequence of Yersinia pestis, the causative agent of plague."  
RL Nature 413:523-527(2001).  
DR EMBL; AJ414156; CAC92624.1; --  
DR PIR; AD0412; AD0412.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR011545; DEAD/DEAH\_N.  
DR InterPro; IPR010225; DEAH\_box\_HrpB.  
DR InterPro; IPR001650; Helicase\_C.  
DR InterPro; IPR007502; Helicase\_dom.  
DR Pfam; PF00270; DEAD; 1.  
DR Pfam; PF04408; HA2; 1.  
DR Pfam; PF00271; Helicase\_C; 1.  
DR PIRSF; PIRSF005496; ATP\_hel\_hrpB; 1.  
DR SMART; SM00487; DEXDC; 1.  
DR SMART; SM00490; HELIC; 1.  
DR TIGRFAMs; TIGR01970; DEAH\_box\_HrpB; 1.  
KW ATP-binding; Complete proteome; Helicase; Hydrolase.  
SQ SEQUENCE 828 AA; 91982 MW; 3A11F88835D5E583 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 828;  
Best Local Similarity 58.3%; Pred. No. 2.4e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10  
||| : |||  
Db 372 CGLWLELLSWG 383

RESULT 3  
Q8D1A7  
ID Q8D1A7 PRELIMINARY; PRT; 853 AA.  
AC Q8D1A7; Q74XU2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Helicase, ATP-dependent.  
GN Name=hrpB; OrderedLocusNames=YPO291, y0794;  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KIM5 / Biovar Mediaevalis;  
RX MEDLINE=22137863; PubMed=12142430;  
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Blattner F.R.,  
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Perry R.D.;  
RT "Genome sequence of Yersinia pestis KIM."

RL J. Bacteriol. 184:4601-4611(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=91001 / Biovar Mediaevalis;  
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,  
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,  
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,  
RA Yang R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE013681; AAM84381.1; --  
DR EMBL; AE017128; AAS60566.1; --  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.  
DR GO; GO:0004386; F:helicase activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR011545; DEAD/DEAH\_N.  
DR InterPro; IPR010225; DEAH\_box\_HrpB.  
DR InterPro; IPR001650; Helicase\_C.  
DR InterPro; IPR007502; Helicase\_dom.  
DR Pfam; PF00270; DEAD; 1.  
DR Pfam; PF04408; HA2; 1.  
DR Pfam; PF00271; Helicase\_C; 1.  
DR PIRSF; PIRSF005496; ATP\_hel\_hrpB; 1.  
DR SMART; SM00487; DEXDC; 1.  
DR SMART; SM00490; HELIC; 1.  
DR TIGRFAMs; TIGR01970; DEAH\_box\_HrpB; 1.  
KW ATP-binding; Helicase; Hydrolase.  
SQ SEQUENCE 853 AA; 95004 MW; B3DB738A18665B42 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 853;  
Best Local Similarity 58.3%; Pred. No. 2.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10  
||| : |||  
Db 397 CGLWLELLSWG 408

RESULT 4  
AAS60566  
ID AAS60566 PRELIMINARY; PRT; 853 AA.  
AC AAS60566;  
DT 24-MAR-2004 (TrEMBLrel. 27, Created)  
DT 24-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 04-MAY-2004 (TrEMBLrel. 27, Last annotation update)  
DE Helicase, ATP-dependent.  
GN HRPB OR YP0291.  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=91001 / Biovar Mediaevalis;  
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,  
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,  
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,  
RA Yang R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE017128; AAS60566.1; --  
KW Helicase.  
SQ SEQUENCE 853 AA; 95004 MW; B3DB738A18665B42 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 853;  
Best Local Similarity 58.3%; Pred. No. 2.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10  
||| : |||  
Db 397 CGLWLELLSWG 408



```
RESULT 5
P90670
ID P90670 PRELIMINARY; PRT; 1993 AA.
AC P90670;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sodium channel alpha-subunit SCAP1.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nervous system;
RX MEDLINE=97238630; PubMed=9115644;
RA Dyer J.R., Johnston W.L., Caetellucci V.F., Dunn R.J.;
RT "Cloning and tissue distribution of the Aplysia Na+ channel alpha-
subunit cDNA.";
RL DNA Cell Biol. 16:347-356(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; U66915; AAC47457.1; -.
DR PIR; T30902; T30902.
DR HSSP; P04775; 1BYX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1993 AA; 225896 MW; 33E174B98F07E1A7 CRC64;

Query Match 60.4%; Score 43.5; DB 2; Length 1993;
Best Local Similarity 54.5%; Pred. No. 8.9e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
Db 942 CGEWIESMWGC 952

RESULT 6
Q6H022
ID Q6H022 PRELIMINARY; PRT; 168 AA.
AC Q6H022;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FD33;
RA Stowe-Evans E.L., Ford J., Kehoe D.M.;
RT "Genomic DNA Microarray Analysis: Identification of New Genes
Regulated by Light Color in the Cyanobacterium Fremyella
diplosiphon.";
```

```
RL J. Bacteriol. 186:4338-4349(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FD33;
RA Stowe-Evans E., Ford J., Kehoe D.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY548455; AAT41947.1; -.
KW Hypothetical protein.
SQ SEQUENCE 168 AA; 18932 MW; 1C9DB963D5210332 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 168;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYWLTIWG 9
Db 122 CGYWLSLRG 130

RESULT 7
Q74JK6
ID Q74JK6 PRELIMINARY; PRT; 221 AA.
AC Q74JK6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN OrderedLocusNames=LJ1101;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017203; AAS08923.1; -.
DR InterPro; IPR004254; HlyIII_related.
DR InterPro; IPR005744; HlyIII.
DR Pfam; PF03006; HlyIII; 1.
DR TIGRFAMs; TIGR01065; hlyIII; 1.
KW Complete proteome.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
Db 172 GFWLLVWG 179

RESULT 8
AAS08923
ID AAS08923 PRELIMINARY; PRT; 221 AA.
AC AAS08923;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN LJ1101.
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
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RP SEQUENCE FROM N.A.  
RC STRAIN=NCC 533;  
RX PubMed=14966310;  
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,  
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,  
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;  
RT "The genome sequence of the probiotic intestinal bacterium  
RT Lactobacillus johnsonii NCC 533.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).  
DR EMBL; AE017203; AAS08923.1; --  
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;  
  
Query Match 59.7%; Score 43; DB 2; Length 221;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 9  
Db 172 GFWLLVWG 179  
  
RESULT 9  
Q6C574 PRELIMINARY; PRT; 501 AA.  
AC Q6C574;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Chromosome E of strain CLIB99 of Yarrowia lipolytica.  
GN ORFNames=YALI0E20471g;  
OS Yarrowia lipolytica (Candida lipolytica).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Dipodascaceae; Yarrowia.  
OX NCBI\_TaxID=4952;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RG GENOLEVURES;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts.";  
RL Nature 430:35-44(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RA Genoscope;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR382131; CAG79783.1; --  
SQ SEQUENCE 501 AA; 56411 MW; 91F08EF5A63C60FB CRC64;  
  
Query Match 59.7%; Score 43; DB 2; Length 501;  
Best Local Similarity 66.7%; Pred. No. 3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GYWLTIWG 10  
Db 157 GYLLTLWYC 165  
  
RESULT 10  
Q8DKD6

ID Q8DKD6 PRELIMINARY; PRT; 646 AA.  
AC Q8DKD6;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tll0923 protein.  
GN OrderedLocusNames=tll0923;  
OS Synechococcus elongatus (Thermosynechococcus elongatus).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=32046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BP-1;  
RX MEDLINE=22225144; PubMed=12240834;  
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,  
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the thermophilic cyanobacterium  
RT Thermosynechococcus elongatus BP-1.";  
RL DNA Res. 9:123-130(2002).  
DR EMBL; AP005372; BAC08475.1; --  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR InterPro; IPR001932; PP2C-like.  
DR Pfam; PF00481; PP2C; 1.  
DR SMART; SM00332; PP2Cc; 1.  
DR SMART; SM00331; PP2C\_SIG; 1.  
KW Complete proteome.  
SQ SEQUENCE 646 AA; 71071 MW; 56C5A74F76652D56 CRC64;  
  
Query Match 59.7%; Score 43; DB 2; Length 646;  
Best Local Similarity 62.5%; Pred. No. 3.7e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 YWLTIWG 10  
Db 415 YWINRWGC 422  
  
RESULT 11  
Q8H2N7 PRELIMINARY; PRT; 733 AA.  
ID Q8H2N7  
AC Q8H2N7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein OJ1138\_B05.118.  
GN Name=OJ1138\_B05.118;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP005486; BAC16197.1; --  
DR Gramene; Q8H2N7; --  
DR InterPro; IPR007658; DUF594.  
DR Pfam; PF04578; DUF594; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;  
  
Query Match 59.7%; Score 43; DB 2; Length 733;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 YWLTIWG 9  
Db 328 YWTTIWG 334

```
RESULT 12
Q7WY20
ID Q7WY20 PRELIMINARY; PRT; 1084 AA.
AC Q7WY20;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RCsC.
GN Name=rcsC; ORFNames=RL038;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA14;
RX PubMed=14983043;
RA He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T.,
RA Lee D., Urbach J., Goodman H.M., Rahme L.G.;
RT "The broad host range pathogen Pseudomonas aeruginosa strain PA14
RT carries two pathogenicity islands harboring plant and animal virulence
RT genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
CC -I- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AY273869; AAP84165.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:000156; F:two-component response regulator activity; IEA.
DR GO; GO:000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR008207; Hpt.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HiskA; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00072; Response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HiskA; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50894; HPT; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase.
SQ SEQUENCE 1084 AA; 119129 MW; C953FDD2F273BF1B CRC64;

Query Match 59.7%; Score 43; DB 2; Length 1084;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWGC 10
Db 750 GAWLKAWGC 758

RESULT 13
Q96AC0
ID Q96AC0 PRELIMINARY; PRT; 152 AA.
AC Q96AC0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGTRAP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match 59.7%; Score 43; DB 2; Length 1084;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWGC 10
Db 750 GAWLKAWGC 758

RESULT 14
Q6RW13
ID Q6RW13 PRELIMINARY; PRT; 159 AA.
AC Q6RW13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Angiotensin II receptor-associated protein.
GN Name=AGTRAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY488088; AAR25556.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR009436; AGTRAP.
DR Pfam; PF06396; AGTRAP; 1.
KW Receptor.
SQ SEQUENCE 159 AA; 17419 MW; 7E1D5C7E79AB6BC5 CRC64;

Query Match 59.0%; Score 42.5; DB 2; Length 159;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 GYW-LTIWGC 10
Db 14 GHWLLTTWGC 23

RESULT 15
Q6RW13
ID Q6RW13 PRELIMINARY; PRT; 159 AA.
AC Q6RW13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Angiotensin II receptor-associated protein.
GN Name=AGTRAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017328; AAH17328.1; -.
DR InterPro; IPR009436; AGTRAP.
DR Pfam; PF06396; AGTRAP; 1.
SQ SEQUENCE 152 AA; 16669 MW; 637C01214175C3C9 CRC64;

Query Match 59.0%; Score 42.5; DB 2; Length 152;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 GYW-LTIWGC 10
Db 14 GHWLLTTWGC 23
```

QY 2 GYW-LTIWGC 10  
|:| | | | |  
Db 14 GHWLLTTWGC 23

RESULT 15  
Q9NRW9 PRELIMINARY; PRT; 159 AA.  
AC Q9NRW9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ATRAP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Ye R.D., He R.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF165187; AAF89547.1; -.  
DR Genew; HGNC:13539; AGTRAP.  
DR InterPro; IPR009436; AGTRAP.  
DR Pfam; PF06396; AGTRAP; 1.  
SQ SEQUENCE 159 AA; 17518 MW; 7E012C7E79AE6BC5 CRC64;

Query Match 59.0%; Score 42.5; DB 2; Length 159;  
Best Local Similarity 70.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 GYW-LTIWGC 10  
|:| | | | |  
Db 14 GHWLLTTWGC 23



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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:42:03 ; Search time 153 Seconds  
(without alignments)  
16.412 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_23Sep04:\*
- 1: geneseqp1980s:\*
  - 2: geneseqp1990s:\*
  - 3: geneseqp2000s:\*
  - 4: geneseqp2001s:\*
  - 5: geneseqp2002s:\*
  - 6: geneseqp2003as:\*
  - 7: geneseqp2003bs:\*
  - 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	84.2	7	5	ABP53964 VEGFR-3 b
2	31	81.6	7	3	AAY76794 Somatosta
3	31	81.6	7	5	ABP53418 Backbone
4	26	68.4	6	2	AAR93713 Cyclo[-Ty
5	25	65.8	7	3	AAY76792 Somatosta
6	25	65.8	7	5	ABP53416 Backbone
7	24	63.2	4	8	ADJ38912 AID targe
8	24	63.2	5	2	AAR76079 MAB 55.1
9	24	63.2	5	3	AAY32257 Light cha
10	24	63.2	5	8	ADM10172 Human pro
11	24	63.2	5	8	ADM10201 Human pro
12	24	63.2	6	2	AAR80643 Receptor
13	24	63.2	6	5	AAU83934 Tyrosine
14	24	63.2	6	6	ABJ37222 Rhodopsin
15	24	63.2	6	6	ABJ37226 Rhodopsin
16	24	63.2	6	6	ABJ37224 Rhodopsin
17	24	63.2	6	8	ABG75386 C melo se
18	24	63.2	7	2	AAR08140 Neurokini
19	24	63.2	7	2	AAR62543 Fibronect
20	24	63.2	7	3	AAY76793 Somatosta
21	24	63.2	7	3	AAU78246 Clonorch
22	24	63.2	7	3	AAU77087 Clonorch
23	24	63.2	7	4	AAM44768 H11 bindi
24	24	63.2	7	4	AAM44793 H11 bindi
25	24	63.2	7	5	AAU81571 Enterokin

26	24	63.2	7	5	ABP53417	Abp53417 Backbone
27	24	63.2	7	5	AAU70373	Aau70373 Mouse hea
28	24	63.2	7	6	ABU79853	Abu79853 Enterokin
29	24	63.2	7	6	AAO26659	Aao26659 Chit36 de
30	24	63.2	7	7	ADD26602	Add26602 BGS-19 pe
31	24	63.2	7	8	ADJ25834	Adj25834 Tyrosine
32	23	60.5	7	2	AAY33139	Aay33139 Rabbit ca
33	22	57.9	5	6	ABR55082	Abr55082 MMP subst
34	22	57.9	5	8	ADK14234	Adk14234 Matrix me
35	22	57.9	6	2	AAR48807	Aar48807 Peptide w
36	22	57.9	6	2	AAR46290	Aar46290 PTP-D1/D2
37	22	57.9	6	2	AAW43021	Aaw43021 Protein t
38	22	57.9	6	3	AAY81787	Aay81787 Protein t
39	22	57.9	7	2	AAy14751	Aay14751 Tyrosine
40	22	57.9	7	2	AAy14752	Aay14752 Tyrosine
41	22	57.9	7	7	ADL17115	Adl17115 Phage-dis
42	22	57.9	7	7	ADL17125	Adl17125 Phage-dis
43	21	55.3	5	2	AAR12680	Aar12680 Pentapept
44	21	55.3	5	2	AAR51544	Aar51544 Mimotope
45	21	55.3	5	2	AAR69912	Aar69912 Pentameri

ALIGNMENTS

RESULT 1  
ABP53964  
ID ABP53964 standard; peptide; 7 AA.  
XX

AC ABP53964;

XX  
DT 09-JAN-2003 (first entry)

XX  
DE VEGFR-3 binding peptide SEQ ID NO:67.

XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytotstatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnerary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.

XX Homo sapiens.

OS Synthetic.

XX  
FH Key Location/Qualifiers

FT Misc-difference 4..6 /note= "X is any amino acid"

XX  
PN WO200257299-A2.

XX  
PD 25-JUL-2002.

XX  
PR 16-JAN-2002; 2002WO-IB0000099.

XX  
PR 17-JAN-2001; 2001US-0262476P.

XX  
PA (LUDW-) LUDWIG INST CANCER RES.

XX  
PA (LICN ) LICENTIA LTD.

XX  
PI Alitalo K, Koivunen E, Kubo H;

XX  
DR WPI; 2002-691521/74.

XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.

XX  
PS Claim 21; Page 81; 149pp; English.

XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,



CC antidiabetic and vulnery activities, and can be used in gene therapy.  
CC .Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 7 AA;

Query Match 84.2%; Score 32; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 1 GYWXXXW 7

RESULT 2  
ID AAY76794 standard; peptide; 7 AA.  
XX AAY76794;  
AC  
XX 20-APR-2000 (first entry)  
DT  
DE Somatostatin analogue peptide 3181.  
XX

KW Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.  
XX  
OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT Misc-difference 3 /note= "D-form residue"  
FT Modified-site 7 /note= "Trp-NH2"  
FT

XX WO9965508-A1.  
XX  
XX 23-DEC-1999.  
PD  
XX 15-JUN-1999; 99WO-IL000329.  
PF  
XX 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
XX  
PA (PEPT-) PEPTOR LTD.  
XX  
XX Hornik V, Afargan MM, Gellerman G;  
PI  
XX WPI; 2000-136888/12.  
DR  
XX Cyclized somatostatin analogs for inhibiting growth hormone secretion  
PT from anterior pituitary and as antiproliferative agents for the treatment  
PT of tumors.  
XX  
XX Example 11; Page 61; 82pp; English.  
PS

XX This sequence represents a somatostatin analogue of the invention. The  
CC invention relates to a backbone cyclised somatostatin analogue that has  
CC one building unit containing a nitrogen atom of the peptide backbone  
CC connected to a bridging group comprising an amide, thioether, thioester

CC or disulphide. At least one building unit is connected via a bridging  
CC group to form a cyclic structure with a moiety selected from a second  
CC building unit, side chain of or N-terminal amino acid residue. A  
CC composition containing the analogue may be used for preventing disorders  
CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
CC associated complications, gastrointestinal disorders, inflammatory  
CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
CC analogue is used for imaging the existence of metastases. Somatostatin  
CC analogues can be used for the treatment of patients with hormone-secreting  
CC and hormone-dependent tumours. They reduce diarrhoea through the  
CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
CC effect on intestinal secretion. Somatostatin analogues selective to type  
CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
CC and restenosis. The analogues are metabolically stable, selective in  
CC their in-vivo activities and safe  
XX  
SQ Sequence 7 AA;

Query Match 81.6%; Score 31; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 1 GYWKVCW 7

RESULT 3  
ID ABP53418 standard; peptide; 7 AA.  
XX  
AC ABP53418;  
XX 19-NOV-2002 (first entry)  
DT  
XX Backbone cyclised somatostatin analogue PTR 3181.  
DE  
XX

KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
KW somatotropin release inhibiting factor; somatostatin receptor subtype;  
KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;  
KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
KW pancreatitis; post-surgical pain.  
XX  
OS Synthetic.  
XX

XX Key Location/Qualifiers  
FH Modified-site 1 /note= "N-terminally modified with Fmoc  
FT (fluorenylmethoxycarbonyl)"  
FT  
FT Misc-difference 3 /note= "D form residue"  
FT Modified-site 7 /note= "amidated"  
FT  
XX  
XX US2002052315-A1.  
XX  
XX 02-MAY-2002.  
PD  
XX 13-DEC-2000; 2000US-00734583.  
PF  
XX 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
PR 15-JUN-1999; 99WO-IL000329.  
XX

XX (HORN/) HORNIK V.  
PA (AFAR/) AFARGAN M M.  
PA (GELL/) GELLERMAN G.  
XX  
PI Hornik V, Afargan MM, Gellerman G;

XX WPI; 2002-681319/73.

XX New backbone cyclized somatostatin analogs are e.g. useful in the

PT treatment of atherosclerosis, autoimmune diseases and cancers.

PT

XX

PS Example 12; Page 21; 30pp; English.

XX

CC The present invention describes backbone cyclised somatostatin analogues

CC (I) that incorporates at least one building unit containing one nitrogen

CC atom of the peptide backbone connected to a bridging group (comprising an

CC amide, thioether, thioester or disulfide) where at least one building

CC unit is connected via the bridging group to form a cyclic structure with

CC a moiety selected from the group consisting of a second building unit,

CC the side chain of an amino acid residue of the sequence or the N-terminal

CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,

CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and

CC can be used as a somatostatin receptor ligand. (I) are useful in the

CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-

CC associated complications, endocrine disorders, inflammation,

CC gastrointestinal disorders, pancreatitis, post-surgical pain, and

CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging

CC the existence of metastases, it being labeled with a detectable probe.

CC The present sequence represents a backbone cyclised somatostatin analogue

CC from the present invention

XX

SQ Sequence 7 AA;

Query Match 81.6%; Score 31; DB 5; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.7e+06;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

Db |||||

1 GYWKVCW 7

RESULT 4

AAR93713

ID AAR93713 standard; peptide; 6 AA.

XX

AC AAR93713;

XX

DT 10-MAY-1996 (first entry)

XX

DE Cyclo[-Tyr-trp-Leu-Arg-Gly-Trp-].

XX

KW neurokinin A antagonist; tachykinin; respiratory disease; asthma;

KW analgesic; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "not an N-terminal amino acid, but condensed with

FT Trp(6) to form a cyclic peptide"

FT Misc-difference 2

FT /note= "D-form residue"

FT Modified-site 6

FT /note= "not a C-terminal amino acid, but condensed with

FT Tyr(1) to form a cyclic peptide"

XX

PN WO9521187-A1.

XX

PD 10-AUG-1995.

XX

XX

PF 10-JAN-1995; 95WO-US000296.

XX

PR 03-FEB-1994; 94US-00191571.

XX

PA (RICH ) MERRELL DOW PHARM INC.

XX

PI Owen TJ, Kudlacz EM, Buck SH, Harbeson SL;

XX WPI; 1995-336695/43.

XX

PT New cyclic peptide derivs. - are neurokinin A and tachykinin antagonists

PT useful e.g. for treating asthma or as analgesics.

XX

PS Claim 8; Page 69; 82pp; English.

XX

CC The patent describes novel cyclic hexapeptide and octapeptide compounds

CC which are antagonists of neurokinin A and which are useful medically as

CC analgesics and for treating respiratory diseases such as asthma. The

CC present sequence represents a specifically preferred example of the new

CC peptides

XX

SQ Sequence 6 AA;

Query Match 68.4%; Score 26; DB 2; Length 6;

Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXXW 7

Db |||||

1 YWLRGW 6

RESULT 5

AAAY76792

ID AAAY76792 standard; peptide; 7 AA.

XX

AC AAAY76792;

XX

DT 20-APR-2000 (first entry)

XX

DE Somatostatin analogue peptide 3177.

XX

KW Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;

KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;

KW gastrointestinal disorder; inflammatory disease; pancreatitis;

KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;

KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;

KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 3 /note= "D-form residue"

FT Modified-site 7 /note= "Trp-NH2"

XX

PN WO9965508-A1.

XX

PD 23-DEC-1999.

XX

PF 15-JUN-1999; 99WO-IL000329.

XX

PR 19-JUN-1998; 98US-00100360.

PR 02-DEC-1998; 98US-00203389.

XX

PA (PEPT-) PEPTOR LTD.

XX

PI Hornik V, Afargan MM, Gellerman G;

XX

XX WPI; 2000-136888/12.

XX

CC Cyclized somatostatin analogs for inhibiting growth hormone secretion

PT from anterior pituitary and as antiproliferative agents for the treatment

PT of tumors.

XX

PS Example 11; Page 61; 82pp; English.

XX

CC This sequence represents a somatostatin analogue of the invention. The

CC invention relates to a backbone cyclised somatostatin analogue that has

CC one building unit containing a nitrogen atom of the peptide backbone  
CC connected to a bridging group comprising an amide, thioether, thioester  
CC or disulphide. At least one building unit is connected via a bridging  
CC group to form a cyclic structure with a moiety selected from a second  
CC building unit, side chain of or N-terminal amino acid residue. A  
CC composition containing the analogue may be used for preventing disorders  
CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
CC associated complications, gastrointestinal disorders, inflammatory  
CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
CC analogue is used for imaging the existence of metastases. Somatostatin  
CC analogues can be used for the treatment of patients with hormone-secreting  
CC and hormone-dependent tumours. They reduce diarrhoea through the  
CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
CC effect on intestinal secretion. Somatostatin analogues selective to type  
CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
CC and restenosis. The analogues are metabolically stable, selective in  
CC their in-vivo activities and safe

XX  
SQ Sequence 7 AA;  
  
Query Match 65.8%; Score 25; DB 3; Length 7;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
|||  
Db 2 YWKVCW 7  
  
RESULT 6  
ABP53416  
ID ABP53416 standard; peptide; 7 AA.  
XX  
AC ABP53416;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Backbone cyclised somatostatin analogue PTR 3177.  
XX  
KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
KW somatotropin release inhibiting factor; somatostatin receptor subtype;  
KW synthesis; antiarteriosclerotic; immunosuppressive; cytotstatic; cancer;  
KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
KW pancreatitis; post-surgical pain.

XX Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 3 /note= "D form residue"  
FT Modified-site 7  
FT /note= "amidated"  
XX  
PN US2002052315-A1.  
XX  
XX  
PD 02-MAY-2002.  
XX  
PF 13-DEC-2000; 2000US-00734583.  
XX  
PR 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
PR 15-JUN-1999; 99WO-IL000329.  
XX  
XX (HORN/) HORNIK V.  
PA (AFAR/) AFARGAN M M.  
PA (GELL/) GELLERMAN G.  
XX  
PI Hornik V, Afargan MM, Gellerman G;  
XX

DR WPI; 2002-681319/73.  
XX New backbone cyclized somatostatin analogs are e.g. useful in the  
PT treatment of atherosclerosis, autoimmune diseases and cancers.  
XX  
PS Example 12; Page 21; 30pp; English.  
XX  
CC The present invention describes backbone cyclised somatostatin analogues  
CC (I) that incorporates at least one building unit containing one nitrogen  
CC atom of the peptide backbone connected to a bridging group (comprising an  
CC amide, thioether, thioester or disulfide) where at least one building  
CC unit is connected via the bridging group to form a cyclic structure with  
CC a moiety selected from the group consisting of a second building unit,  
CC the side chain of an amino acid residue of the sequence or the N-terminal  
CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,  
CC cytotstatic, antidiabetic, antiinflammatory and analgesic activities, and  
CC can be used as a somatostatin receptor ligand. (I) are useful in the  
CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-  
CC associated complications, endocrine disorders, inflammation,  
CC gastrointestinal disorders, pancreatitis, post-surgical pain, and  
CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging  
CC the existence of metastases, it being labeled with a detectable probe.  
CC The present sequence represents a backbone cyclised somatostatin analogue  
CC from the present invention  
XX  
SQ Sequence 7 AA;

Query Match 65.8%; Score 25; DB 5; Length 7;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
|||  
Db 2 YWKVCW 7  
  
RESULT 7  
ADJ38912  
ID ADJ38912 standard; peptide; 4 AA.  
XX  
AC ADJ38912;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE AID target hotspot motif peptide, SEQ ID 9.  
XX  
KW Anti-HIV; Cytostatic; Immunostimulant; Gene Therapy; Vaccine;  
KW HIV TAT protein transduction domain; human; CEM15; hemagglutinin domain;  
KW AID; activation induced deaminase; enzyme.  
XX  
OS Unidentified.  
XX  
PN WO2004013160-A2.  
XX  
PD 12-FEB-2004.  
XX  
PF 05-AUG-2003; 2003WO-US024458.  
XX  
PR 05-AUG-2002; 2002US-0401293P.  
PR 21-OCT-2002; 2002US-0419982P.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Smith HC, Sowden MP, Dewhurst S, Kim B, Wedekind J;  
XX  
XX WPI; 2004-169321/16.

XX New chimeric protein useful for treating human immunodeficiency virus  
PT infection in a subject, comprises protein transduction domain and a  
PT cytidine deaminase domain.

PS Disclosure; SEQ ID NO 9; 240pp; English.

XX

CC The present invention relates to chimeric proteins (I) which comprise a  
CC protein transduction domain and a deaminase domain. In (I), the protein  
CC transduction domain is chosen from poly-arginine, poly-lysine peptide,  
CC third alpha-helix of Antennapedia homeodomain protein, HSV-1 virion  
CC protein (VP)22, HIV-1 Vpr and HIV TAT protein. The deaminase domain  
CC comprises CEM15 or Activation Induced Deaminase (AID). (I) further  
CC comprises an epitope tag which is a hemagglutinin or a polyhistidine tag,  
CC and a polypeptide domain that enhances solubility of (I). (I) further  
CC comprises a third polypeptide comprising a cytoplasmic localization  
CC protein (e.g. chicken muscle pyruvate kinase) or its fragment which  
CC enhances localization of the chimeric protein to the cytoplasm. (I) is  
CC useful for interrupting HIV infectivity which involves contacting an HIV-  
CC infected cell or a cell prior to HIV infection with (I) to allow delivery  
CC of (I) into the cell, where (I) binds with vif to interrupt HIV  
CC infectivity, for treating a subject with an HIV infection or at risk for  
CC an HIV infection which involves administering (I) to the subject, where  
CC the administration step is dose-dependent or transient. (I) is also  
CC useful for treating a subject for hyper-IgM syndrome which involves  
CC administering (I) to a subject exhibiting hyper-IgM syndrome, where (I)  
CC taken up by B lymphocyte cells induces antibody production sufficient to  
CC treat the hyper-IgM syndrome. (I) is useful for treating a subject for B  
CC lymphocyte cell lymphoma which involves administering (I) to a subject  
CC exhibiting B lymphocyte cell lymphoma, where (I) is taken up by cancerous  
CC B lymphocyte cells, and inhibits blunt cell growth, thus treating the  
CC lymphoma. (I) is also useful for treating conditions such as cancer and  
CC infectious diseases. The present sequence was used to illustrate the  
CC invention.  
XX  
SQ Sequence 4 AA;

Query Match 63.2%; Score 24; DB 8; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 2 GYW 4

RESULT 8  
AAR76079  
ID AAR76079 standard; peptide; 5 AA.

XX AAR76079;

DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)

DE MAB 55.1 heavy chain CDR1.

XX Antigen binding structure; complementarity determining region; CDR;  
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.

XX Mus sp.

XX WO9515382-A1.

XX 08-JUN-1995.

XX 29-NOV-1994; 94WO-GB002610.

XX 03-DEC-1993; 93GB-00024819.

PR 03-JUN-1994; 94GB-00011089.

XX (ZENE ) ZENECA LTD.

XX Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
PI Blakey DC;

XX WPI; 1995-215262/28.

XX Antigen binding structures containing CDR's recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
PT and therapy of cancer.  
XX Claim 2; Page 96; 121pp; English.  
PS An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
XX of the heavy and light chains of MAB 55.1 (ECCACC 93081901), which  
CC recognises the colorectal tumor-associated antigen CA55.1. It is  
CC optionally humanized and in the form F(ab')<sub>2</sub>, F(ab)' , Fab, Fv, scFv or V-  
CC min, and is produced in transgenic animals or plants. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

XX Sequence 5 AA;

Query Match 63.2%; Score 24; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 1 GYW 3

RESULT 9  
AAY32257  
ID AAY32257 standard; peptide; 5 AA.

XX AAY32257;

DT 15-FEB-2000 (first entry)

DE Light chain CDR H1 of mouse anti-CD23 MAB C11.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
KW therapy.

XX Mus musculus.

XX WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

PR 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

DR N-PSDB; AAZ34742.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
PT diabetes, multiple sclerosis and psoriasis.

XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 1 (CDR H1)  
CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
CC (see also AAY32263). The invention provides altered antibodies, such as  
CC chimeric or humanised antibodies, which comprise sufficient of the amino  
CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to



CC render them capable of binding to the CD23 type II molecule expressed on  
CC haematopoietic cells. The antibodies are used to block soluble CD23  
CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
CC are also useful for studying interactions between CD23 and various  
CC ligands and determining the binding agents  
XX  
SQ Sequence 5 AA;  
  
Query Match 63.2%; Score 24; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
Db |||  
1 GYW 3  
  
RESULT 10  
ADM10172  
ID ADM10172 standard; peptide; 5 AA.  
XX  
AC ADM10172;  
DT  
DT 20-MAY-2004 (first entry)  
XX  
DE Human proteome unique recognition sequence (URS) seqid 496.  
XX  
KW soluble peptide analyte; unique recognition sequence; URS;  
KW protein detection; clinical diagnosis; environmental diagnosis;  
KW drug discovery; protein sequencing; pathogen detection; toxin detection;  
KW anthrax toxin; small pox toxin; cholera toxin;  
KW packaged protein detection array; protein expression profile;  
KW drug screening; protein characterisation; disease prognosis;  
KW pathologic cell profiling; proteome epitope tag; human; proteome.  
XX  
OS Homo sapiens.  
XX  
PN US2004038307-A1.  
XX  
PD 26-FEB-2004.  
XX  
PF 12-MAY-2003; 2003US-00436549.  
XX  
PR 10-MAY-2002; 2002US-0379626P.  
PR 01-JUL-2002; 2002US-0393137P.  
PR 01-JUL-2002; 2002US-0393197P.  
PR 01-JUL-2002; 2002US-0393211P.  
PR 01-JUL-2002; 2002US-0393223P.  
PR 01-JUL-2002; 2002US-0393233P.  
PR 01-JUL-2002; 2002US-0393235P.  
PR 01-JUL-2002; 2002US-0393280P.  
PR 04-DEC-2002; 2002US-0430948P.  
PR 13-DEC-2002; 2002US-0433319P.  
XX  
PA (ENGE-) ENGINEOS INC.  
XX  
PI Lee FD, Meng X, Chan JW, Zhang S, Benkovic SJ;  
XX  
XX WPI; 2004-327083/30.  
DR  
XX  
PT Detecting proteins comprises providing solution of soluble peptide  
PT analytes, contacting solution with capture agents capable of interacting  
PT with unique recognition sequence of protein and detecting binding between  
PT agents and analytes.  
XX  
PS Claim 60; SEQ ID NO 496; 134pp; English.

XX  
CC The invention describes a method of detecting proteins in sample. The  
CC method comprises: providing a solution of soluble peptide analytes  
CC produced by denaturation and/or cleavage of several sample proteins, and  
CC optionally, labeling the collection of peptides by a detectable part;  
CC contacting the solution with one or more capture agent(s), where each of  
CC the capture agent(s) is able to specifically recognise and interact with  
CC a unique recognition sequence (URS) of a reference protein; and detecting  
CC the binding between one or more of the capture agent(s) and the peptide  
CC analytes, where the detection of binding between a capture agent and a  
CC peptide analyte indicates the presence of the reference protein in the  
CC several of sample proteins. Also described are; a method of protein in the  
CC quantifying proteins in a biological sample; a method of simultaneously  
CC detecting several specific proteins in a multi-protein sample. The method  
CC of the invention is used in clinical or environmental diagnosis, drug  
CC discovery, protein sequencing and for the detection of a pathogen or  
CC toxins (such as anthrax toxin, small pox toxin, and cholera toxin). A  
CC packaged protein detection array is useful for: quantifying various forms  
CC of post-translationally modified proteins in a biological sample;  
CC screening large libraries of natural or synthetic compounds to identify  
CC competitors of natural or non-natural ligands for the capture agent,  
CC which may be of diagnostic, prognostic, therapeutic or scientific  
CC interest; and to study the relationship between a subject protein  
CC expression profile and that subjects response to a foreign compound or  
CC drug. The methods of assaying differential protein expression are useful  
CC in the identification and validation of new potential drug targets as  
CC well as for drug screening. The capture agents are useful for protein  
CC characterisation, for screening, making prognosis of disease outcomes and  
CC providing treatment modality suggestion based on the profiling of the  
CC pathologic cells, prognosis of the outcome of a normal lesion and  
CC susceptibility of lesions to malignant transformation. The methods  
CC described are useful for identifying and/or detecting a specific organism  
CC based on the organisms proteome epitope tag. This is the amino acid  
CC sequence of a human proteome unique recognition sequence (URS).  
XX  
SQ Sequence 5 AA;  
  
Query Match 63.2%; Score 24; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
Db |||  
1 GYW 3  
  
RESULT 11  
ADM10201  
ID ADM10201 standard; peptide; 5 AA.  
XX  
AC ADM10201;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human proteome unique recognition sequence (URS) seqid 525.  
XX  
KW soluble peptide analyte; unique recognition sequence; URS;  
KW protein detection; clinical diagnosis; environmental diagnosis;  
KW drug discovery; protein sequencing; pathogen detection; toxin detection;  
KW anthrax toxin; small pox toxin; cholera toxin;  
KW packaged protein detection array; protein expression profile;  
KW drug screening; protein characterisation; disease prognosis;  
KW pathologic cell profiling; proteome epitope tag; human; proteome.  
XX  
OS Homo sapiens.  
XX  
PN US2004038307-A1.  
XX  
PD 26-FEB-2004.  
XX  
PF 12-MAY-2003; 2003US-00436549.  
XX  
PR 10-MAY-2002; 2002US-0379626P.



PR 01-JUL-2002; 2002US-0393137P.  
PR 01-JUL-2002; 2002US-0393197P.  
PR 01-JUL-2002; 2002US-0393211P.  
PR 01-JUL-2002; 2002US-0393223P.  
PR 01-JUL-2002; 2002US-0393233P.  
PR 01-JUL-2002; 2002US-0393235P.  
PR 01-JUL-2002; 2002US-0393280P.  
PR 04-DEC-2002; 2002US-0430948P.  
PR 13-DEC-2002; 2002US-0433319P.  
XX  
PA (ENGE-) ENGINEOS INC.  
PI Lee FD, Meng X, Chan JW, Zhang S, Benkovic SJ;  
XX  
DR WPI; 2004-327083/30.  
XX  
PT Detecting proteins comprises providing solution of soluble peptide  
PT analytes, contacting solution with capture agents capable of interacting  
PT with unique recognition sequence of protein and detecting binding between  
PT agents and analytes.  
XX  
PS Claim 60; SEQ ID NO 525; 134pp; English.  
XX  
CC The invention describes a method of detecting proteins in sample. The  
CC method comprises: providing a solution of soluble peptide analytes  
CC produced by denaturation and/or cleavage of several sample proteins, and  
CC optionally, labeling the collection of peptides by a detectable part;  
CC contacting the solution with one or more capture agent(s), where each of  
CC the capture agent(s) is able to specifically recognise and interact with  
CC a unique recognition sequence (URS) of a reference protein; and detecting  
CC the binding between one or more of the capture agent(s) and the peptide  
CC analytes, where the detection of binding between a capture agent and a  
CC peptide analyte indicates the presence of the reference protein in the  
CC several of sample proteins. Also described are; and a method of  
CC quantifying proteins in a biological sample; a method of simultaneously  
CC detecting several specific proteins in a multi-protein sample. The method  
CC of the invention is used in clinical or environmental diagnosis, drug  
CC discovery, protein sequencing and for the detection of a pathogen or  
CC toxins (such as anthrax toxin, small pox toxin, and cholera toxin). A  
CC packaged protein detection array is useful for: quantifying various forms  
CC of post-translationally modified proteins in a biological sample;  
CC screening large libraries of natural or synthetic compounds to identify  
CC competitors of natural or non-natural ligands for the capture agent,  
CC which may be of diagnostic, prognostic, therapeutic or scientific  
CC interest; and to study the relationship between a subject protein  
CC expression profile and that subjects response to a foreign compound or  
CC drug. The methods of assaying differential protein expression are useful  
CC in the identification and validation of new potential drug targets as  
CC well as for drug screening. The capture agents are useful for protein  
CC characterisation, for screening, making prognosis of disease outcomes and  
CC providing treatment modality suggestion based on the profiling of the  
CC pathologic cells, prognosis of the outcome of a normal lesion and  
CC susceptibility of lesions to malignant transformation. The methods  
CC described are useful for identifying and/or detecting a specific organism  
CC based on the organisms proteome epitope tag. This is the amino acid  
CC sequence of a human proteome unique recognition sequence (URS).  
XX  
SQ Sequence 5 AA;  
  
Query Match 63.2%; Score 24; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
Db ||| 2 GYW 4  
  
RESULT 12  
AAR80643  
ID AAR80643 standard; peptide; 6 AA.  
XX  
AC AAR80643;

XX 25-MAR-2003 (revised)  
DT 05-MAR-1996 (first entry)  
XX  
DE Receptor binding peptide used in a new isolation method.  
XX  
KW Protease; vaccine; isolation; diagnosis; receptor; bacteriophage;  
KW oligonucleotide library.  
XX  
OS Synthetic.  
XX  
PN US5432018-A.  
XX  
PD 11-JUL-1995.  
XX  
PF 20-JUN-1991; 91US-00718577.  
XX  
PR 20-JUN-1990; 90US-00541108.  
XX  
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
XX  
PI Barrett RW, Cwirla SE, Dower WJ;  
XX  
DR WPI; 1995-254429/33.  
XX  
PT Identification of phage encoding a substrate for a specific protease -  
PT useful for identification of peptide(s) potentially useful as vaccines,  
PT therapeutic or diagnostic agents.  
XX  
PS Example 3; Col 29; 28pp; English.  
XX  
CC AAR80638-R80659 are peptides identified using a new method of peptide  
CC detection which involves the use of a pre-selected receptor to which the  
CC peptides bind. The peptides are isolated by screening libraries which may  
CC be very large. The dissociation rate of the individual peptides can be  
CC obtained as a measure of the amt. of receptor that binds to each isolate  
CC as a function of time. The method is used to identify peptides that are  
CC potentially useful as vaccines or as therapeutic or diagnostic agents,  
CC i.e. able to bind the pre-selected receptor and act as an agonist or  
CC antagonist. The new method enables peptides to be isolated without prior  
CC knowledge of their ligand or receptor structure. (Updated on 25-MAR-2003  
CC to correct PF field.)  
XX  
SQ Sequence 6 AA;  
  
Query Match 63.2%; Score 24; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
Db ||| 2 GYW 4  
  
RESULT 13  
AAU83934  
ID AAU83934 standard; peptide; 6 AA.  
XX  
AC AAU83934;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Tyrosine recombinase inhibitory peptide #37.  
XX  
KW Tyrosine recombinase; antibacterial; cytostatic; cell growth modulator;  
KW site-specific DNA recombinase; type I DNA topoisomerase; tumour;  
KW tyrosine recombinase; cancer; Holliday junction.  
XX  
OS Synthetic.  
XX  
PN WO200198540-A2.  
XX  
PD 27-DEC-2001.

XX PF 21-JUN-2001; 2001WO-US020046.  
XX PR 22-JUN-2000; 2000US-00602087.  
XX PA (UYSA-) UNIV SAN DIEGO STATE FOUND.  
XX PI Segall A, Pinilla C;  
XX DR WPI; 2002-114591/15.  
XX PT Identifying cell growth modulators for inhibiting cancer cell growth in humans, involves assessing and comparing activity of site-specific recombinase or type I DNA topoisomerase in presence/absence of test substance.  
XX PS Claim 39; Page 90; 115pp; English.  
XX CC The method relates to a method of identifying a modulator of cell growth, comprising assessing and comparing the activities of site-specific DNA recombinase (I) or type I DNA topoisomerase (II) in presence and absence of a test substance. A difference in activity of (I) and (II) assessed in the presence and absence of the test substance indicates that the test substance modulates cell growth. The identified cell growth modulator, preferably an inhibitor of (I) or (II), is useful for inhibiting cell growth in a subject, preferably a human. The inhibitor inhibits (I) which is preferably tyrosine recombinase or type I DNA topoisomerase in humans having or suspected of having tumour or cancer, where the method further involves administering an effective of antitumour or anticancer agent or treatment; or who are, or are suspected of being infected by a bacterium, in which case the inhibitor inhibits Holliday junction intermediate resolution activity of tyrosine recombinase. The method further involves administering an effective amount of antibiotic or antibacterium treatment. AAU83898-AAU83991 represents tyrosine recombinase inhibitory peptides of the invention  
XX SQ Sequence 6 AA;  
Query Match 63.2%; Score 24; DB 5; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 YWXXW 7  
Db 1 YWCYWW 6  
RESULT 14  
ABJ37222  
ID ABJ37222 standard; peptide; 6 AA.  
XX AC ABJ37222;  
XX DT 08-MAY-2003 (first entry)  
XX DE Rhodopsin related G-protein coupled receptor binding site peptide #98.  
XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR; Rhodopsin.  
XX OS Unidentified.  
XX PN WO2003004147-A2.  
XX PD 16-JAN-2003.  
XX PR 05-JUL-2002; 2002WO-GB003094.  
XX PF 06-JUL-2001; 2001GB-00016570.  
XX PA (BIOF-) BIOFOCUS PLC.  
XX PI Crossley R, Rose VS, Stevens AP;

XX DR WPI; 2003-221549/21.  
XX PT Producing compound library, by generating biological target model using target sequence information, defining microenvironments interacting with ligand and motifs interacting with microenvironment, and assembling motifs.  
XX PS Disclosure; Fig 1; 39pp; English.  
XX CC The invention relates to a novel method for producing a compound library. The novel method involves reducing a biological target into a group of one or more amino acids required for interaction with a ligand, to generate a model of the biological target, using the model to define a microenvironment in the biological target, capable of interacting with the ligand, defining motifs which interact with the microenvironment, and assembling the motifs to generate a compound library for screening. The novel method is useful to produce compound libraries for screening natural ligands such as peptides and proteins or for producing chemical compounds based on drug motifs for screening. This sequence represents a peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin, which relates to the novel compound library production method of the invention  
XX SQ Sequence 6 AA;  
Query Match 63.2%; Score 24; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYW 3  
Db 4 GYW 6  
RESULT 15  
ABJ37226  
ID ABJ37226 standard; peptide; 6 AA.  
XX AC ABJ37226;  
XX DT 08-MAY-2003 (first entry)  
XX DE Rhodopsin related G-protein coupled receptor binding site peptide #102.  
XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR; Rhodopsin.  
XX OS Unidentified.  
XX PN WO2003004147-A2.  
XX PD 16-JAN-2003.  
XX PR 05-JUL-2002; 2002WO-GB003094.  
XX PR 06-JUL-2001; 2001GB-00016570.  
XX PA (BIOF-) BIOFOCUS PLC.  
XX PI Crossley R, Rose VS, Stevens AP;  
XX DR WPI; 2003-221549/21.  
XX PT Producing compound library, by generating biological target model using target sequence information, defining microenvironments interacting with ligand and motifs interacting with microenvironment, and assembling motifs.  
XX PS Disclosure; Fig 1; 39pp; English.  
XX CC The invention relates to a novel method for producing a compound library. The novel method involves reducing a biological target into a group of

CC one or more amino acids required for interaction with a ligand, to  
CC generate a model of the biological target, using the model to define a  
CC microenvironment in the biological target capable of interacting with the  
CC ligand, defining motifs which interact with the microenvironment, and  
CC assembling the motifs to generate a compound library for synthesis. The  
CC novel method is useful to produce compound libraries for screening  
CC natural ligands such as peptides and proteins or for producing chemical  
CC compounds based on drug motifs for screening. This sequence represents a  
CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,  
CC which relates to the novel compound library production method of the  
CC invention

XX

SQ Sequence 6 AA;

Query Match 63.2%; Score 24; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3

|||

Db 4 GYW 6

Search completed: December 29, 2004, 22:04:19  
Job time : 156 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:56:54 ; Search time 36 Seconds  
(without alignments)  
12.895 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	63.2	5	1 US-08-353-400-27	Sequence 27, Appl
2	24	63.2	5	4 US-08-753-750B-38	Sequence 38, Appl
3	24	63.2	5	6 5185431-15	Patent No. 5185431
4	24	63.2	6	1 US-07-718-577-6	Sequence 6, Appli
5	24	63.2	7	1 US-07-973-235A-30	Sequence 30, Appl
6	24	63.2	7	1 US-08-443-640-16	Sequence 16, Appl
7	24	63.2	7	2 US-08-462-720-30	Sequence 30, Appl
8	24	63.2	7	4 US-09-388-788-2	Sequence 2, Appli
9	24	63.2	7	4 US-09-069-827A-94	Sequence 94, Appl
10	24	63.2	7	4 US-09-563-222C-53	Sequence 53, Appl
11	22	57.9	6	2 US-08-446-345-12	Sequence 12, Appl
12	22	57.9	6	3 US-08-951-260A-2	Sequence 2, Appli
13	22	57.9	6	3 US-08-884-569A-11	Sequence 11, Appl
14	22	57.9	6	3 US-08-884-569A-14	Sequence 14, Appl
15	22	57.9	6	4 US-09-430-626A-2	Sequence 2, Appli
16	22	57.9	6	4 US-09-361-096A-46	Sequence 46, Appl
17	22	57.9	6	4 US-09-743-492A-5	Sequence 5, Appli
18	22	57.9	6	4 US-10-243-687-2	Sequence 2, Appli
19	22	57.9	7	2 US-08-652-971-5	Sequence 5, Appli
20	22	57.9	7	2 US-08-991-258A-5	Sequence 5, Appli
21	22	57.9	7	2 US-08-769-399-5	Sequence 5, Appli
22	22	57.9	7	3 US-08-991-953A-5	Sequence 5, Appli
23	21	55.3	5	6 5217869-38	Patent No. 5217869
24	21	55.3	7	3 US-09-082-279B-653	Sequence 653, App
25	21	55.3	7	3 US-09-315-304B-653	Sequence 653, App
26	21	55.3	7	3 US-09-315-304B-1579	Sequence 1579, Ap
27	21	55.3	7	4 US-09-350-325-39	Sequence 39, Appl

28	21	55.3	7	4 US-09-834-784-653	Sequence 653, App
29	21	55.3	7	4 US-09-515-965A-653	Sequence 653, App
30	21	55.3	7	4 US-09-350-641C-653	Sequence 653, App
31	21	55.3	7	4 US-09-350-641C-1579	Sequence 1579, Ap
32	21	55.3	7	4 US-09-350-841A-653	Sequence 653, App
33	20	52.6	5	2 US-08-480-434-22	Sequence 22, Appl
34	20	52.6	5	2 US-08-480-434-31	Sequence 31, Appl
35	20	52.6	5	2 US-08-053-451B-22	Sequence 22, Appl
36	20	52.6	5	2 US-08-053-451B-31	Sequence 31, Appl
37	20	52.6	5	6 5217869-8	Patent No. 5217869
38	20	52.6	5	6 5217869-14	Patent No. 5217869
39	20	52.6	6	1 US-07-718-577-2	Sequence 2, Appli
40	20	52.6	6	1 US-07-718-577-10	Sequence 10, Appl
41	20	52.6	6	1 US-07-973-235A-29	Sequence 29, Appl
42	20	52.6	6	1 US-08-487-006-67	Sequence 67, Appl
43	20	52.6	6	1 US-08-487-006-88	Sequence 88, Appl
44	20	52.6	6	2 US-08-462-720-29	Sequence 29, Appl
45	20	52.6	6	2 US-08-488-659A-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1  
US-08-353-400-27  
; Sequence 27, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,400  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9324819.3  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9411089.7  
; FILING DATE: 03-JUN-1994  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-353-400-27  
  
Query Match 63.2%; Score 24; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GYW 3  
|||  
Db 1 GYW 3  
  
RESULT 2  
US-08-753-750B-38  
; Sequence 38, Application US/08753750B  
; Patent No. 6610506  
; GENERAL INFORMATION:  
; APPLICANT: Io, Reggie Y.C.  
; APPLICANT: Schryvers, Anthony B.  
; APPLICANT: Potter, Andrew A.  
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF



;  
;  
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME  
;  
; FILE REFERENCE: A34762 021645.0105  
;  
; CURRENT APPLICATION NUMBER: US/08/753,750B  
;  
; CURRENT FILING DATE: 1996-11-29  
;  
; PRIOR APPLICATION NUMBER: CA 2,164,274  
;  
; PRIOR FILING DATE: 1995-12-01  
;  
; PRIOR APPLICATION NUMBER: 60/008,569  
;  
; PRIOR FILING DATE: 1995-12-01  
;  
; NUMBER OF SEQ ID NOS: 68  
;  
; SOFTWARE: FastSEQ for Windows Version 4.0  
;  
; SEQ ID NO 38  
;  
; LENGTH: 5  
;  
; TYPE: PRT  
;  
; ORGANISM: Pasteurella haemolytica  
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US-08-753-750B-38

Query Match 63.2%; Score 24; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 3 GYW 5

RESULT 3  
5185431-15  
;Patent No. 5185431  
; APPLICANT: YOSHIMATSU, KENTARO;SHIKATA, YASUSHI;TANAKA, ISAO;  
;HASEGAWA, YOSHIKAZU;SETO, TOSHIO;OSAWA, TOSHIO  
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR  
;  
; NUMBER OF SEQUENCES: 31  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/392,841  
; FILING DATE: 11-AUG-1989  
;SEQ ID NO:15:  
; LENGTH: 5  
5185431-15

Query Match 63.2%; Score 24; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
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Db 2 GYW 4

RESULT 4  
US-07-718-577-6  
; Sequence 6, Application US/07718577  
; Patent No. 5432018  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Barrett, Ronald W.  
; TITLE OF INVENTION: PEPTIDE LIBRARY AND  
; TITLE OF INVENTION: SCREENING SYSTEMS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Street  
; STREET: Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

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;  
; APPLICATION NUMBER: US/07/718,577  
;  
; FILING DATE: 19910620  
;  
; CLASSIFICATION: 435  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/541,108  
; FILING DATE: 20-JUN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11509-25-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
;  
US-07-718-577-6

Query Match 63.2%; Score 24; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 2 GYW 4

RESULT 5  
US-07-973-235A-30  
; Sequence 30, Application US/07973235A  
; Patent No. 5491130  
; GENERAL INFORMATION:  
; APPLICANT: David D. Roberts, et al.  
; TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and  
; TITLE OF INVENTION: Related Collagen-Binding Proteins  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lowe, Price, LeBlanc & Becker  
; STREET: Suite 300, 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect, Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/973,235A  
; FILING DATE: 19921110  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robert L. Price  
; REGISTRATION NUMBER: 22,685  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)684-1111  
; TELEFAX: (703)684-1124  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: AMINO ACIDS  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
;  
US-07-973-235A-30

Query Match 63.2%; Score 24; DB 1; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05;

Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
| | | |  
Db 1 GGWSKSW 7

RESULT 6  
US-08-443-640-16  
; Sequence 16, Application US/08443640  
; Patent No. 5691140  
; GENERAL INFORMATION:  
; APPLICANT: NOREN, CHRISTOPHER J.  
; APPLICANT: EVANS, PAUL D.  
; TITLE OF INVENTION: BIDIRECTIONAL IN VITRO TRANSCRIPTION  
; TITLE OF INVENTION: VECTORS UTILIZING A SINGLE RNA POLYMERASE FOR BOTH  
; TITLE OF INVENTION: DIRECTIONS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEW ENGLAND BIOLABS, INC  
; STREET: 32 TOZER ROAD  
; CITY: BEVERLY  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,640  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILLIAMS, GREGORY D.  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: NEB-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 927-5054  
; TELEFAX: (508) 927-1705  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-443-640-16

Query Match 63.2%; Score 24; DB 1; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
| | | |  
Db 1 GEWRFW 7

RESULT 7  
US-08-462-720-30  
; Sequence 30, Application US/08462720  
; Patent No. 5849701  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, David D.  
; APPLICANT: Kruttsch, Henry C.  
; APPLICANT: Sipes, John M.  
; APPLICANT: Guo, Neng-hua  
; APPLICANT: Negre, Eric  
; TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and  
; TITLE OF INVENTION: Related Collagen-Binding Proteins  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,720  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 015280-023110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-462-720-30

Query Match 63.2%; Score 24; DB 2; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
| | | |  
Db 1 GGWSKSW 7

RESULT 8  
US-09-388-788-2  
; Sequence 2, Application US/09388788  
; Patent No. 6429359  
; GENERAL INFORMATION:  
; APPLICANT: LAMPPA, GAYLE  
; TITLE OF INVENTION: PRODUCTION OF CELLULASE IN PLASTIDS OF TRANSGENIC  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 21459/90301  
; CURRENT APPLICATION NUMBER: US/09/388,788  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein  
; OTHER INFORMATION: Construct  
US-09-388-788-2

Query Match 63.2%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
| | |  
Db 5 GYW 7

RESULT 9  
US-09-069-827A-94

; Sequence 94, Application US/09069827A  
; Patent No. 6617114  
; GENERAL INFORMATION:  
; APPLICANT: FOWLKES, Dana M  
; KAY, Brian K  
; FRELINGER, Jeffrey A  
; HYDE-DERUYSCHE, Robin P  
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING  
; COMPLEMENTARY COMBINATORIAL LIBRARIES

; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 624 Ninth Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069,827A  
; FILING DATE: 30-Apr-1998  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/050,359  
; FILING DATE: 31-MAR-1998  
; APPLICATION NUMBER: PCT/US97/19638  
; FILING DATE: 31-OCT-1997  
; APPLICATION NUMBER: US 08/740,671  
; FILING DATE: 31-OCT-1996

; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOWLKES=4C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:

US-09-069-827A-94  
  
Query Match 63.2%; Score 24; DB 4; Length 7;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXXW 7  
|||  
Db 1 YWWPDW 6

RESULT 10  
US-09-563-222C-53  
; Sequence 53, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/09/563,222C  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222C-53

Query Match 63.2%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 2 GYW 4

RESULT 11  
US-08-446-345-12  
; Sequence 12, Application US/08446345  
; Patent No. 5831009  
; GENERAL INFORMATION:  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Moller, Niels P.H.  
; APPLICANT: Moller, Karin B.  
; TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASES PTP-D1  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: N.Y.  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,345  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/234,440  
; FILING DATE: 28-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30742  
; REFERENCE/DOCKET NUMBER: 7683-054  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-446-345-12

Query Match 57.9%; Score 22; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YWXXXW 7  
:|||  
Db 1 FWXXW 6

RESULT 12  
US-08-951-260A-2  
; Sequence 2, Application US/08951260A  
; Patent No. 6004791  
; GENERAL INFORMATION:  
; APPLICANT: Aoki, Naohito  
; APPLICANT: Ullrich, Axel  
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/951,260A  
; FILING DATE: October 16, 1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030,860  
; FILING DATE: No. 6004791ember 13, 1996  
; APPLICATION NUMBER: PCT/1897/00946  
; FILING DATE: June 17, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 227/004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: "Xaa" in positions 3 and 5 stand  
; OTHER INFORMATION: for an unspecified amino acid.  
US-08-951-260A-2

Query Match 57.9%; Score 22; DB 3; Length 6;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
:| | |  
Db 1 FWXXW 6

RESULT 13  
US-08-884-569A-11  
; Sequence 11, Application US/08884569A  
; Patent No. 6399326  
; GENERAL INFORMATION:  
; APPLICANT: CHIANG, MING-KO  
; APPLICANT: FLANAGAN, JOHN G.  
; TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO  
; FILE REFERENCE: HMV-020.01

; CURRENT APPLICATION NUMBER: US/08/884,569A  
; CURRENT FILING DATE: 1997-06-27  
; PRIOR APPLICATION NUMBER: 60/021,040  
; PRIOR FILING DATE: 1996-07-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: Ile or Val  
; US-08-884-569A-11

Query Match 57.9%; Score 22; DB 3; Length 6;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
:| | |  
Db 1 FWRMXW 6

RESULT 14  
US-08-884-569A-14  
; Sequence 14, Application US/08884569A  
; Patent No. 6399326  
; GENERAL INFORMATION:  
; APPLICANT: CHIANG, MING-KO  
; APPLICANT: FLANAGAN, JOHN G.  
; TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO  
; FILE REFERENCE: HMV-020.01  
; CURRENT APPLICATION NUMBER: US/08/884,569A  
; CURRENT FILING DATE: 1997-06-27  
; PRIOR APPLICATION NUMBER: 60/021,040  
; PRIOR FILING DATE: 1996-07-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)  
; OTHER INFORMATION: Arg or Gln  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: Ile or Val  
; US-08-884-569A-14

Query Match 57.9%; Score 22; DB 3; Length 6;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
:| | |  
Db 1 FWXXW 6

RESULT 15  
US-09-430-626A-2  
; Sequence 2, Application US/09430626A  
; Patent No. 6482605  
; GENERAL INFORMATION:  
; APPLICANT: Aoki, Naohito  
; APPLICANT: Ullrich, Axel





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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:01:50 ; Search time 141 Seconds  
(without alignments)  
17.859 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXXW 7  
  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
  
Searched: 1599051 seqs, 35972711 residues  
Total number of hits satisfying chosen parameters: 60586

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
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16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	84.2	7	13	US-10-046-922-67
2	24	63.2	5	15	US-10-436-549-496
3	24	63.2	5	15	US-10-436-549-525
4	24	63.2	5	16	US-10-712-425-496
5	24	63.2	5	16	US-10-712-425-525
6	24	63.2	6	15	US-10-418-943-48
7	24	63.2	6	16	US-10-346-737A-45
8	24	63.2	7	9	US-09-884-767A-38
9	24	63.2	7	10	US-09-563-222-53
10	24	63.2	7	15	US-10-403-938-27
11	24	63.2	7	16	US-10-475-853-6
12	24	63.2	7	17	US-10-783-950-53
13	23	60.5	7	17	US-10-858-271-10

14	22	57.9	5	15	US-10-243-613-84	Sequence 84, Appl
15	22	57.9	6	13	US-10-087-993-1	Sequence 1, Appli
16	22	57.9	6	14	US-10-243-687-2	Sequence 2, Appli
17	22	57.9	6	14	US-10-314-232-46	Sequence 46, Appl
18	22	57.9	7	14	US-10-190-082-65	Sequence 65, Appl
19	22	57.9	7	14	US-10-190-082-76	Sequence 76, Appl
20	21	55.3	6	14	US-10-012-456A-48	Sequence 48, Appl
21	21	55.3	7	14	US-10-052-578-195	Sequence 195, App
22	21	55.3	7	14	US-10-347-562-39	Sequence 39, Appl
23	21	55.3	7	14	US-10-053-520-195	Sequence 195, App
24	21	55.3	7	14	US-10-351-641-653	Sequence 653, App
25	21	55.3	7	14	US-10-351-641-1579	Sequence 1579, Ap
26	21	55.3	7	14	US-10-053-498B-195	Sequence 195, App
27	21	55.3	7	15	US-10-258-146A-53	Sequence 53, Appl
28	21	55.3	7	15	US-10-328-953-198	Sequence 198, App
29	21	55.3	7	16	US-10-258-144-88	Sequence 88, Appl
30	20	52.6	6	14	US-10-190-082-39	Sequence 39, Appl
31	20	52.6	6	14	US-10-190-082-126	Sequence 126, App
32	20	52.6	6	14	US-10-190-082-144	Sequence 144, App
33	20	52.6	7	9	US-09-873-676-97	Sequence 97, Appl
34	20	52.6	7	9	US-09-873-676-98	Sequence 98, Appl
35	20	52.6	7	14	US-10-040-394-2	Sequence 2, Appli
36	20	52.6	7	14	US-10-190-082-19	Sequence 19, Appl
37	20	52.6	7	14	US-10-190-082-33	Sequence 33, Appl
38	20	52.6	7	14	US-10-190-082-42	Sequence 42, Appl
39	20	52.6	7	14	US-10-190-082-68	Sequence 68, Appl
40	20	52.6	7	14	US-10-190-082-88	Sequence 88, Appl
41	20	52.6	7	14	US-10-190-082-95	Sequence 95, Appl
42	20	52.6	7	14	US-10-190-082-100	Sequence 100, App
43	20	52.6	7	14	US-10-190-082-109	Sequence 109, App
44	20	52.6	7	14	US-10-190-082-136	Sequence 136, App
45	20	52.6	7	14	US-10-190-082-145	Sequence 145, App

ALIGNMENTS

RESULT 1  
US-10-046-922-67  
; Sequence 67, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046, 922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X at position 4-6 is any amino acid  
US-10-046-922-67

Query Match 84.2%; Score 32; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
| | | | |  
Db 1 GYWXXXW 7

RESULT 2  
US-10-436-549-496  
; Sequence 496, Application US/10436549



Qy 1 GYW 3  
|||  
Db 1 GYW 3

RESULT 5  
US-10-712-425-525  
; Sequence 525, Application US/10712425  
; Publication No. US20040180380A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, FRANK D.  
; APPLICANT: MENG, XUN  
; APPLICANT: LIVINGSTON, DAVID  
; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN  
; FILE REFERENCE: ENGE-P02-001  
; CURRENT APPLICATION NUMBER: US/10/712,425  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 525  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-712-425-525

Query Match 63.2%; Score 24; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 2 GYW 4

RESULT 6  
US-10-418-943-48  
; Sequence 48, Application US/10418943  
; Publication No. US20040002441A1  
; GENERAL INFORMATION:  
; APPLICANT: Segall, Anca  
; APPLICANT: Pinilla, Clemencia  
; TITLE OF INVENTION: RECOMBINATION MODULATORS AND METHODS  
; FILE REFERENCE: 011443 008-999  
; CURRENT APPLICATION NUMBER: US/10/418,943  
; CURRENT FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: 09/602,087  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 48  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-418-943-48

Query Match 63.2%; Score 24; DB 15; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXXW 7  
|||  
Db 1 YWCYWW 6

RESULT 7  
US-10-346-737A-45  
; Sequence 45, Application US/10346737A  
; Publication No. US20040142379A1  
; GENERAL INFORMATION:  
; APPLICANT: St. Hilaire, Phaedria  
; TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS  
; FILE REFERENCE: 11225.16US01  
; CURRENT APPLICATION NUMBER: US/10/346,737A  
; CURRENT FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-10-346-737A-45

Query Match 63.2%; Score 24; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 4 GYW 6

RESULT 8  
US-09-884-767A-38  
; Sequence 38, Application US/09884767A  
; Publication No. US20020192789A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX Corp.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Luneau, Christopher J.  
; APPLICANT: Ladner, Robert C  
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
; CURRENT APPLICATION NUMBER: US/09/884,767A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 09/597,321  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
US-09-884-767A-38

Query Match 63.2%; Score 24; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
Db 1 GYW 3

RESULT 9  
US-09-563-222-53  
; Sequence 53, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-53

Query Match 63.2%; Score 24; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
Db 2 GYW 4

RESULT 10  
US-10-403-938-27  
; Sequence 27, Application US/10403938  
; Publication No. US20040025195A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,  
; TITLE OF INVENTION: BGS-19  
; FILE REFERENCE: D0227 NP  
; CURRENT APPLICATION NUMBER: US/10/403,938  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368,422  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-938-27

Query Match 63.2%; Score 24; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
Db 3 GYW 5

RESULT 11  
US-10-475-853-6  
; Sequence 6, Application US/10475853  
; Publication No. US20040121442A1  
; GENERAL INFORMATION:  
; APPLICANT: Chet, ilan  
; APPLICANT: Viterbo, Ada  
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING  
; TITLE OF INVENTION: PROMOTERS OF SAME AND USES THEREOF

; FILE REFERENCE: 27049  
; CURRENT APPLICATION NUMBER: US/10/475,853  
; CURRENT FILING DATE: 2003-11-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide derived from chit36  
US-10-475-853-6

Query Match 63.2%; Score 24; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
Db 1 GYW 3

RESULT 12  
US-10-783-950-53  
; Sequence 53, Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783,950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-783-950-53

Query Match 63.2%; Score 24; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
Db 2 GYW 4

RESULT 13  
US-10-858-271-10  
; Sequence 10, Application US/10858271  
; Publication No. US20040259829A1  
; GENERAL INFORMATION:  
; APPLICANT: Danks, Mary K.  
; APPLICANT: Potter, Philip M.  
; APPLICANT: Houghton, Peter J.  
; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of  
; TITLE OF INVENTION: Tumor Cells  
; FILE REFERENCE: SJ-0005  
; CURRENT APPLICATION NUMBER: US/10/858,271  
; CURRENT FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US/09/595,682  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/075,258







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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:57:34 ; Search time 38 Seconds  
(without alignments)  
17.724 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYXXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	52.6	5	2 JH0253	gut pentapeptide -
2	15	39.5	6	2 PT0532	T-cell receptor be
3	14	36.8	6	2 B35640	cerebellar degener
4	14	36.8	6	2 PT0629	T-cell receptor be
5	14	36.8	7	2 S21230	dermorphin (Trp-4,
6	14	36.8	7	2 PT0728	T-cell receptor be
7	14	36.8	7	2 S33567	tubulin beta-3 cha
8	13	34.2	4	2 S09478	globulin IV alpha
9	13	34.2	6	2 A61411	ameletin - rat
10	13	34.2	7	1 A61324	dermorphin - Rohde
11	13	34.2	7	2 A60139	fatty-acid synthas
12	13	34.2	7	2 S71870	glutathione transf
13	13	34.2	7	2 S36662	dermorphin (Lys-7)
14	11	28.9	3	3 F37196	bradykinin-potenti
15	11	28.9	4	2 A34626	RPCH-related neuro
16	11	28.9	4	2 B53284	T-cell receptor be
17	11	28.9	4	2 PT0661	T-cell receptor be
18	11	28.9	5	2 A32516	cholecystokinin-5
19	11	28.9	5	2 A60803	neuropeptide - sea
20	11	28.9	5	2 PT0281	Ig heavy chain CRD
21	11	28.9	5	2 PT0308	Ig heavy chain CRD
22	11	28.9	5	2 PT0729	T-cell receptor be
23	11	28.9	5	2 PT0580	bradykinin-potenti
24	11	28.9	5	2 G37196	alcohol dehydrogen
25	11	28.9	6	2 S66195	dnaA protein - pse
26	11	28.9	6	2 B34835	dihydrofolate redu
27	11	28.9	6	2 A31263	dihydrofolate redu
28	11	28.9	6	2 B31263	T-cell receptor be
29	11	28.9	6	2 PT0519	

30	11	28.9	6	2 PT0637	T-cell receptor be
31	11	28.9	6	2 PT0641	T-cell receptor be
32	11	28.9	6	2 PT0726	T-cell receptor be
33	11	28.9	6	2 F41946	T-cell receptor ga
34	11	28.9	6	2 PD0028	pev-kinin 2 - pena
35	11	28.9	6	2 A61068	locustakinin - mig
36	11	28.9	6	4 I79564	hypothetical TCL3
37	11	28.9	7	2 S09652	hypothetical prote
38	11	28.9	7	2 PQ0727	H2 class I protein
39	11	28.9	7	2 E48394	glycoprotein compo
40	11	28.9	7	2 PH1602	Ig H chain V-D-J r
41	11	28.9	7	2 PT0526	T-cell receptor be
42	11	28.9	7	2 PT0628	T-cell receptor be
43	11	28.9	7	2 PT0642	T-cell receptor be
44	11	28.9	7	2 PT0722	T-cell receptor be
45	11	28.9	7	2 PT0688	T-cell receptor be

ALIGNMENTS

RESULT 1

JH0253  
gut pentapeptide - Japanese eel  
C;Species: Anguilla japonica (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755  
A;Accession: JH0253  
A;Molecule type: protein  
A;Residues: 1-5 <UES>  
A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric , and of the circular muscle of the gastro-intestinal junction.

Query Match 52.6%; Score 20; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	GYW 3
		:
Db	1	GFW 3

RESULT 2

PT0532  
T-cell receptor beta chain V-D-J region (100-4AJ) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0532  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0532  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: adult thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 39.5%; Score 15; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GYW 3
Db	4	GNW 6

RESULT 3  
B35640  
cerebellar degeneration-related protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 24-Jun-1993  
C;Accession: B35640  
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990  
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker  
A;Reference number: A35640; MUID:90222173; PMID:2326268  
A;Accession: B35640  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-6 <CHE>  
  
Query Match 36.8%; Score 14; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YW 3  
 :|  
Db 1 FW 2  
  
RESULT 4  
PT0629  
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0629; PT0528  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0629  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH  
A;Accession: PT0528  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FE2>  
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB  
C;Keywords: T-cell receptor  
  
Query Match 36.8%; Score 14; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
 :|  
Db 3 GDW 5  
  
RESULT 5  
S21230  
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
C;Accession: S21230  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S21230  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
  
Query Match 36.8%; Score 14; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YW 3  
 :|  
Db 3 FW 4  
  
RESULT 6  
PT0728  
T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0728  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0728  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor  
  
Query Match 36.8%; Score 14; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
 :|  
Db 3 GDW 5  
  
RESULT 7  
S33567  
tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)  
C;Species: Drosophila melanogaster  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C;Accession: S33567  
R;Hinze, U.; Wolk, A.; Renkawitz-Pohl, R.  
Development 116, 543-554, 1992  
A;Title: Ultrabithorax is a regulator of beta-3 tubulin expression in the Drosophila vis  
A;Reference number: S33567; MUID:93170162; PMID:1363225  
A;Accession: S33567  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <HIN>  
A;Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g4377448  
C;Genetics:  
A;Gene: FlyBase:beta-Tub60D  
A;Cross-references: FlyBase:FBgn0003888  
A;Introns: 5/3  
  
Query Match 36.8%; Score 14; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YW 3  
 :|  
Db 6 FW 7  
  
RESULT 8  
S09478  
globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)  
N;Alternate names: 11S globulin alpha subunit gamma chain  
C;Species: Cucurbita sp. (cucurbit)  
C;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 08-Nov-1996  
C;Accession: S09478  
R;Ohmiya, M.; Hara, I.; Matsubara, H.  
Plant Cell Physiol. 21, 157-167, 1980  
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and  
A;Reference number: S09066

A;Accession: S09478  
A;Molecule type: protein  
A;Residues: 1-4 <OHM>

Query Match 34.2%; Score 13; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 3 GY 4

RESULT 9  
A61411  
ameletin - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C;Accession: A61411  
R;Burzynski, S.R.

Anal. Biochem. 70, 359-365, 1976  
A;Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the s  
A;Reference number: A61411; MUID:76182447; PMID:1267130  
A;Accession: A61411

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <BUR>  
C;Superfamily: unassigned animal peptides  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 34.2%; Score 13; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 3 GY 4

RESULT 10  
A61324  
dermorphin - Rohde's leaf frog  
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C;Date: 17-Jul-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C;Accession: A61324  
R;Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.  
Int. J. Pept. Protein Res. 17, 316-321, 1981  
A;Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz  
A;Reference number: A61324; MUID:82029915; PMID:7287302  
A;Accession: A61324  
A;Molecule type: protein  
A;Residues: 1-7 <MON>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
C;Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin  
F;2/Modified site: D-alanine (Ala) #status experimental  
F;6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F;7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 34.2%; Score 13; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 4 GY 5

RESULT 11  
A60139  
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 26-May-2000

C;Accession: A60139  
R;Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.  
Biochim. Biophys. Acta 828, 380-382, 1985  
A;Title: Amino acid sequence around the reactive serine residue of the thioesterase domain  
A;Reference number: A60139; MUID:85175165; PMID:3921056  
A;Accession: A60139  
A;Molecule type: protein  
A;Residues: 1-7 <HAR>

C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homol  
ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-n  
C;Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enz  
F;5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 34.2%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 3 GY 4

RESULT 12  
S71870  
glutathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)  
N;Alternate names: glutathione S-transferase class mu 9  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 07-May-1999  
C;Accession: S71870  
R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.  
Biochem. J. 317, 879-884, 1996  
A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospra  
A;Reference number: S71864; MUID:96332484; PMID:8760377  
A;Accession: S71870  
A;Molecule type: protein  
A;Residues: 1-7 <ROU>

C;Comment: At least five species-independent classes of cytosolic glutathion transferase  
s mitochondrial form are known.  
C;Complex: dimer  
C;Function:  
A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v  
A;Pathway: detoxification; xenobiotics metabolism  
A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism  
es of damage  
C;Superfamily: glutathione transferase  
C;Keywords: acetylated amino end; blocked amino end; dimer; transferase  
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 34.2%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 5 GY 6

RESULT 13  
S36662  
dermorphin (lys-7) [validated] - two-colored leaf frog  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 10-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
C;Accession: S36662  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S36662  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>

C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 34.2%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
|  
Db 4 GY 5

RESULT 14  
F37196  
bradykinin-potentiating peptide 6 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: F37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: F37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-3 <CIN>  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.9%; Score 11; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 3 W 3

RESULT 15  
A34626  
RPCH-related neuropeptide - ferruginous spindle  
C;Species: Fusinus ferrugineus (ferruginous spindle)  
C;Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 31-Dec-1993  
C;Accession: A34626  
R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;  
Biochem. Biophys. Res. Commun. 167, 273-279, 1990  
A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.  
A;Reference number: A34626; MUID:90179762; PMID:2310394  
A;Accession: A34626  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-4 <KUR>  
C;Keywords: neuropeptide

Query Match 28.9%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 4 W 4



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:43:03 ; Search time 188 Seconds  
(without alignments)  
21.424 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	50.0	5	1 UF01 MOUSE	P38639 mus musculus
2	16	42.1	7	2 Q9BRY4	Q9bry4 homo sapien
3	15	39.5	4	1 OCP3 OCTMI	P58649 octopus min
4	11	28.9	2	1 GWA SEPOF	P83570 sepia offic
5	11	28.9	5	1 BPP7 BOTIN	P30425 bothrops in
6	11	28.9	6	1 EI01 LITRU	P82096 litoria rub
7	11	28.9	6	1 LOK1 LOCM1	P41491 locusta mig
8	11	28.9	7	1 BRHP CONIM	P58803 conus imper
9	11	28.9	7	1 TPFY PACDA	P83455 pachymedusa
10	11	28.9	7	1 TY51 LITRU	P82065 litoria rub
11	11	28.9	7	1 WWA1 ACHFU	P35919 achatina fu
12	11	28.9	7	1 WWA2 ACHFU	P35920 achatina fu
13	11	28.9	7	1 WWA3 ACHFU	P35921 achatina fu
14	11	28.9	7	2 Q95945	Q95945 saccharomyc
15	11	28.9	7	2 O49223	O49223 glycine max
16	11	28.9	7	2 Q8GL00	Q8gl00 borrelia bu
17	11	28.9	7	2 Q8GL04	Q8gl04 borrelia bu
18	11	28.9	7	2 Q8KMS9	Q8kms9 enterobacte
19	11	28.9	7	2 Q8JEB1	Q8je81 human immun
20	10	26.3	5	1 PAP2 PARMA	P81864 pardachirus
21	10	26.3	5	1 RE32 LITRU	P82073 litoria rub
22	9	23.7	4	1 ACHI ACHFU	P35904 achatina fu
23	9	23.7	4	1 OCP1 OCTMI	P58648 octopus min
24	8	21.1	3	1 GRWM HUMAN	P01157 homo sapien
25	8	21.1	4	1 DCML PSECH	P19916 pseudomonas
26	8	21.1	7	2 P82445	P82445 nicotiana t
27	7	18.4	4	1 FAR3 HIRME	P42562 hirudo medi
28	7	18.4	4	1 FAR4 HIRME	P42563 hirudo medi
29	7	18.4	4	1 FYRI ANTEL	P58706 anthopleura
30	7	18.4	4	2 Q96AT0	Q96at0 homo sapien
31	7	18.4	5	1 AL14 CARMA	P81817 carcinus ma

32	7	18.4	5	1 FARP ARTTR	P41853 artiopeathi
33	7	18.4	5	1 PRCT PERAM	P01373 periplaneta
34	7	18.4	5	1 PSK DAUCA	P58261 daucus caro
35	7	18.4	6	1 ASP2 LACSN	P82655 lactobacill
36	7	18.4	6	1 OVM LEPDE	P42985 leptinotars
37	7	18.4	7	1 ALL2 CARMA	P81805 carcinus ma
38	7	18.4	7	1 ALL3 CARMA	P81806 carcinus ma
39	7	18.4	7	1 ALL4 CARMA	P81807 carcinus ma
40	7	18.4	7	1 ALL5 CARMA	P81808 carcinus ma
41	7	18.4	7	1 ALL7 CYDPO	P82158 cydia pomon
42	7	18.4	7	1 ASCL ALLAS	P84071 allium asca
43	7	18.4	7	1 EI05 LITRU	P82101 litoria rub
44	7	18.4	7	1 FAR2 ASCSU	P31890 ascaris suu
45	7	18.4	7	1 FAR3 HAECO	P81298 haemonchus

ALIGNMENTS

RESULT 1  
UF01\_MOUSE STANDARD; PRT; 5 AA.  
AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=75231108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familiar and novel murine proteins using  
RT preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 6.6, its MW is: 19 kDa.

KW Direct protein sequencing.

FT NON TER 5

SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 50.0%; Score 19; DB 1; Length 5;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 WXXXW 7

Db 1 WIGRW 5

RESULT 2

Q9BRY4 PRELIMINARY; PRT; 7 AA.  
ID Q9BRY4  
AC Q9BRY4;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE SQSTM1 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., MCEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC005857; AAH05857.3; --  
DR GO; GO:0005829; C:cytosol; ISS.  
DR GO; GO:0019901; F:protein kinase binding; ISS.  
DR GO; GO:0042169; F:SH2 domain binding; ISS.  
DR GO; GO:0043130; F:ubiquitin binding; ISS.  
DR GO; GO:0016197; P:endosome transport; ISS.  
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.  
DR GO; GO:0045944; P:positive regulation of transcription from P. . .; ISS.  
DR GO; GO:0008104; P:protein localization; ISS.  
DR GO; GO:0043122; P:regulation of I-kappaB kinase/NF-kappaB cas. . .; ISS.  
DR GO; GO:0006950; P:response to stress; ISS.  
DR InterPro; IPR000449; UBA.  
DR InterPro; IPR000433; Znf\_ZZ.  
DR Pfam; PF00569; ZZ; 1.  
DR SMART; SM00165; UBA; 1.  
DR SMART; SM00291; Znf\_ZZ; 1.  
DR PROSITE; PS50030; UBA; 1.  
DR PROSITE; PS01357; ZF\_ZZ\_1; UNKNOWN\_1.  
DR PROSITE; PS50135; ZF\_ZZ\_2; 1.  
SQ SEQUENCE 7 AA; 779 MW; 737728769DDDD6F0 CRC64;  
  
Query Match 42.1%; Score 16; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
Db 5 GLW 7  
  
RESULT 3  
OCP3\_OCTMI STANDARD; PRT; 4 AA.  
AC P58649;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cardioactive peptides Ocp-3/Ocp-4.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=89766;  
RN [1]  
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10876044;  
RA Iwakoshi E., Hisada M., Minakata H.;  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor.";  
RL Peptides 21:623-630(2000).  
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and

CC inotropic effects on the heart. Ocp-4 is a 1000 time less active  
CC than Ocp-3.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
KW D-amino acid; Direct protein sequencing; Hormone.  
FT MOD RES 2 2 D-serine (in form Ocp-4).  
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;  
  
Query Match 39.5%; Score 15; DB 1; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
Db 1 GSW 3  
  
RESULT 4  
GWA\_SEPOF STANDARD; PRT; 2 AA.  
ID - GWA SEPOF  
AC P83570;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide Gwa.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX MEDLINE=98100358; PubMed=9437704;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
RT peptide inhibiting the motility of the mature oviduct in the  
RT cuttlefish, Sepia officinalis.";  
RL Peptides 18:1469-1474(1997).  
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity  
CC targeting the distal oviduct. Inhibits the motility of the oviduct  
CC by decreasing tonus, frequency and amplitude of contractions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 2 2 Tryptophan amide.  
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 2 W 2  
  
RESULT 5  
BPP7\_BOTIN STANDARD; PRT; 5 AA.  
ID -BPP7 BOTIN  
AC P30425;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Venom; MEDLINE=90351557; PubMed=2386615;  
RX Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RA "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it. It acts  
CC as an indirect hypotensive agent.  
DR PIR; G37196; G37196.  
KW Direct protein sequencing; Hypotensive agent;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
SQ SEQUENCE 5 AA; 629 MW; 776DC373226B00000 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 3 W 3  
  
RESULT 6  
EI01\_LITRU STANDARD; PRT; 6 AA.  
ID EI01\_LITRU  
AC P82096;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litori electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing.  
FT MOD\_RES 6 6 Methionine amide.  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 5 W 5  
  
RESULT 7  
LOK1\_LOCMI STANDARD; PRT; 6 AA.  
ID LOK1\_LOCMI  
AC P41491;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Locustakinin I.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca; MEDLINE=92262851; PubMed=1585017;  
RX Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
RA de Loof A.;  
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
RT isolation, primary structure and synthesis.";  
RL Regul. Pept. 37:49-57(1992).  
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation  
CC of ion transport and inhibition of diuretic activity in Malpighian  
CC tubules.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR; A61068; A61068.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 6 6 Glycine amide.  
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 5 W 5  
  
RESULT 8  
BRHP\_CONIM STANDARD; PRT; 7 AA.  
ID BRHP\_CONIM  
AC P58803;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bromheptapeptide Im.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=97184108; PubMed=9030520;  
RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,  
RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
RA McIntosh J.M.;  
RT "A novel post-translational modification involving bromination of  
RT tryptophan. Identification of the residue, L-6-bromotryptophan, in  
RT peptides from Conus imperialis and Conus radiatus venom.";  
RL J. Biol. Chem. 272:4689-4698(1997).  
CC -!- FUNCTION: Does not elicit gross behavioral symptoms when injected  
CC centrally or peripherally in mice.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=853.19; METHOD=LSI; RANGE=1-7; NOTE=Ref.1.  
DR PIR; A58512; A58512.  
KW Amidation; Bromination; Direct protein sequencing;  
KW Pyrrolidone carboxylic acid.  
FT DISULFID 2 7  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 6 6 6'-bromotryptophan.  
FT MOD\_RES 7 7 Cysteine amide.  
SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 6 W 6

RESULT 9  
TPFY\_PACDA STANDARD; PRT; 7 AA.  
AC P83455;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tryptophyllin-1 (Pdt-1).  
OS Pachymedusa dactinolor (Giant mexican leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
OC Phyllomedusinae; Pachymedusa.  
OX NCBI\_TaxID=75988;  
RN [1]  
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.  
RC TISSUE=Skin secretion;  
RA Chen T.B., Orr D.F., Shaw C.;  
RT "Pachymedusa dactinolor tryptophyllin-1 (pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA.";  
RL Submitted (SEP-2002) to Swiss-Prot.  
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing; Hydroxylation.  
FT MOD\_RES 3 3 Hydroxyproline.  
FT MOD\_RES 7 7 Proline amide.  
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred.No.1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 5 W 5  
  
RESULT 10  
TY51\_LITRU STANDARD; PRT; 7 AA.  
AC P82065;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tryptophyllin 5.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australin red tree frog 'Litoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: May act as a neuromodulator or neurotransmitter.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -!- MASS SPECTROMETRY: MW=965; METHOD=FAB; RANGE=1-7; NOTE=Ref.1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;

KW Neuropeptide; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 7 7 Arginine amide.  
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred.No.1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 4 W 4  
  
RESULT 11  
WWA1\_ACHFU STANDARD; PRT; 7 AA.  
AC P35919;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Wwamide-1.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
CC -!- FUNCTION: Exhibits modulatory effects on the peripheral nervous system. Inhibits activity on a central neuron.  
CC PIR; S33245; S33245.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 7 7 Tryptophan amide.  
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;  
  
Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred.No.1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 W 3  
Db 1 W 1  
  
RESULT 12  
WWA2\_ACHFU STANDARD; PRT; 7 AA.  
AC P35920;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Wwamide-2.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
CC PIR; S33246; S33246.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 7 7 Tryptophan amide.



SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 1 W 1

RESULT 13  
WWA3 ACHFV STANDARD; PRT; 7 AA.  
ID WWA3 ACHFV  
AC P35921;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE WWamide-3.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108 (1993).  
DR PIR; S33244; S33244.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 7 Tryptophan amide.  
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 1 W 1

RESULT 14  
Q95945 PRELIMINARY; PRT; 7 AA.  
ID Q95945  
AC Q95945;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Inside intron 5 (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system: Structure and  
nucleotide sequence of the gene coding for subunit 1 of yeast  
cytochrome oxidase.";  
RL J. Biol. Chem. 255:11927-11941(1980).  
DR EMBL; V00694; CAA24066.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 28.9%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 4 W 4

RESULT 15  
O49223 PRELIMINARY; PRT; 7 AA.  
ID O49223  
AC O49223;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HMG-1-like protein (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Roots;  
RX MEDLINE=91367679; PubMed=1891369;  
RA Laux T., Goldberg R.B.;  
RT "A plant DNA binding protein shares highly conserved sequence motifs  
with HMG-box proteins.";  
RL Nucleic Acids Res. 19:4769-4769 (1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Roots;  
RA Mahalingam R., Knap H.T.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF047050; AAC03556.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match 28.9%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 2 W 2

Search completed: December 29, 2004, 22:07:31  
Job time : 189 secs



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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 48.7358 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	10	4 AAB99759	Aab99759 Rhesus D
2	34	89.5	12	4 AAB99769	Aab99769 Rhesus D
3	34	89.5	452	4 AAU03644	Aau03644 Group B S
4	34	89.5	466	6 ABU21589	Abu21589 Protein e
5	34	89.5	472	6 ABU38334	Abu38334 Protein e
6	34	89.5	474	6 ABU24881	Abu24881 Protein e
7	34	89.5	475	5 ABP30560	Abp30560 Streptoco
8	34	89.5	475	6 ABU40245	Abu40245 Protein e
9	34	89.5	475	6 ABU29756	Abu29756 Protein e
10	34	89.5	478	7 ADC97241	Adc97241 E. faeciu
11	34	89.5	479	5 ABP26968	Abp26968 Streptoco
12	34	89.5	490	5 ABB55389	Abb55389 Lactococc
13	34	89.5	496	5 ABB55385	Abb55385 Lactococc
14	34	89.5	499	7 ABO74582	Abu74582 Pseudomon
15	34	89.5	506	6 ABU22414	Abu22414 Protein e
16	34	89.5	585	7 ADA49403	Ada49403 Multi-epi
17	34	89.5	585	8 ADO24081	Ado24081 Epigene c
18	34	89.5	865	7 ABO70593	Abu70593 Pseudomon
19	33	86.8	10	5 ABP53931	Abp53931 VEGFR-3 b
20	33	86.8	10	5 ABP53932	Abp53932 VEGFR-3 b
21	33	86.8	69	4 AAO13595	Aao13595 Human pol
22	33	86.8	116	2 AAR15437	Aar15437 Heavy cha
23	33	86.8	116	6 ABO27261	Abu27261 ICAM-1 bi
24	33	86.8	116	6 ABO27269	Abu27269 ICAM-1 bi
25	33	86.8	116	6 ABO27263	Abu27263 ICAM-1 bi

26	33	86.8	116	6 ABO27259	Abo27259 ICAM-1 bi
27	33	86.8	116	6 ABO27255	Abo27255 ICAM-1 bi
28	33	86.8	116	6 ABO27277	Abo27277 Humanised
29	33	86.8	116	6 ABO27273	Abo27273 Murine 1A
30	33	86.8	116	6 ABO27257	Abo27257 ICAM-1 bi
31	33	86.8	116	6 ABO27271	Abo27271 ICAM-1 bi
32	33	86.8	116	6 ABO27267	Abo27267 ICAM-1 bi
33	33	86.8	117	6 ABO27265	Abo27265 ICAM-1 bi
34	33	86.8	118	7 ADJ95639	Adj95639 Insulin-1
35	33	86.8	119	8 ADL11890	Adl11890 CDR trans
36	33	86.8	119	8 ADL11886	Adl11886 Chimera a
37	33	86.8	120	4 AAB62747	Aab62747 Human HIV
38	33	86.8	137	7 ADJ95626	Adj95626 Rat insul
39	33	86.8	138	3 AAY77591	Aay77591 Anti-huma
40	33	86.8	138	3 AAY77595	Aay77595 Anti-huma
41	33	86.8	138	4 AAB78864	Aab78864 Anti-huma
42	33	86.8	138	4 AAB78860	Aab78860 Anti-huma
43	33	86.8	163	7 ABM73967	Abm73967 DNA clone
44	33	86.8	227	6 ABU36339	Abu36339 Protein e
45	33	86.8	240	2 AAR15443	Aar15443 Single ch

ALIGNMENTS

RESULT 1  
AAB99759  
ID AAB99759 standard; peptide; 10 AA.  
XX

AC AAB99759;

XX  
DT 21-SEP-2001 (first entry)

XX  
DE Rhesus D antibody binding peptide SEQ ID NO:4.

XX  
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP;  
KW idiopathic thrombocytopaenic purpura; immunoglobulin.

XX  
OS Homo sapiens.

XX  
PN EP1106625-A1.

XX  
PD 13-JUN-2001.

XX  
PF 17-NOV-1999; 99EP-00122858.

XX  
PR 17-NOV-1999; 99EP-00122858.

XX  
PA (ZLBB-) ZLB BIOPLASMA AG.

XX  
PI Miescher S, Hofmann A, Fisch I;

XX  
DR WPI; 2001-383568/41.

XX  
PT Novel peptides capable of binding Rhesus D antibodies are used to  
PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the  
PT newborn (HDN).

XX  
PS Claim 1; Page 12; 19pp; English.

XX  
CC The present sequence represents a peptide capable of binding Rhesus D  
CC antibodies (I). Also described in the present invention are: (1) a  
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
CC (II) operably linked to an expression control system; (3) a cell (IV)  
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
CC peptides having immunologic properties of Rhesus D protein epitopes  
CC comprising subjecting an antibody/antibody fragment recognising an  
CC epitope of Rhesus D protein to several panning rounds with a phage  
CC display library, and identifying immunogenic peptide sequences which are  
CC mimotopes which differ in their amino acid sequence from the amino acid

CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
CC with foreign erythrocytes thereby avoiding the risk of transmission of  
CC viral diseases like AIDS and hepatitis B  
XX  
SQ Sequence 10 AA;  
  
Query Match 89.5%; Score 34; DB 4; Length 10;  
Best Local Similarity 57.1%; Pred. No. 9.9;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 1 GYWSAKW 7  
  
RESULT 2  
AAB99769  
ID AAB99769 standard; peptide; 12 AA.  
XX AAB99769;  
AC  
XX  
DT 21-SEP-2001 (first entry)  
XX  
DE Rhesus D antibody related peptide #5.  
XX  
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;  
KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 1. .12  
XX  
PN EP1106625-A1.  
XX  
PD 13-JUN-2001.  
XX  
PF 17-NOV-1999; 99EP-00122858.  
XX  
PR 17-NOV-1999; 99EP-00122858.  
XX  
PA (ZLBB-) ZLB BIOPLASMA AG.  
XX  
PI Miescher S, Hofmann A, Fisch I;  
XX  
DR WPI; 2001-383568/41.  
XX  
PT Novel peptides capable of binding Rhesus D antibodies are used to  
PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the  
PT newborn (HDN).  
XX  
PS Example 1; Page 8; 19pp; English.  
XX  
CC The present invention describes peptides capable of binding Rhesus D  
CC antibodies (I). Also described in the present invention are: (1) a  
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
CC (II) operably linked to an expression control system; (3) a cell (IV)  
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
CC peptides having immunologic properties of Rhesus D protein epitopes  
CC comprising subjecting an antibody/antibody fragment recognising an  
CC epitope of Rhesus D protein to several panning rounds with a phage  
CC display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid  
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
CC with foreign erythrocytes thereby avoiding the risk of transmission of  
CC viral diseases like AIDS and hepatitis B. The present sequence represents  
CC an anti-Rhesus D (RhD) antibody related peptide which is used in an  
CC example from the present invention  
XX  
SQ Sequence 12 AA;  
  
Query Match 89.5%; Score 34; DB 4; Length 12;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 2 GYWSAKW 8  
  
RESULT 3  
AAU03644  
ID AAU03644 standard; protein; 452 AA.  
XX  
AC AAU03644;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Group B Streptococcus antigenic protein, ID-119.  
XX  
KW Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;  
KW meningitis; neonate; antigenic; vaccine; infection; genital tract;  
KW capsid polysaccharide vaccination.  
XX  
OS Streptococcus agalactiae.  
XX  
PN WO200132882-A2.  
XX  
PD 10-MAY-2001.  
XX  
PF 07-SEP-2000; 2000WO-GB003437.  
XX  
PR 07-SEP-1999; 99GB-00021125.  
XX  
PA (MICR-) MICROBIAL TECHNICS LTD.  
XX  
PI Le Page RWF, Wells JM, Hanniffy SB;  
XX  
DR WPI; 2001-316444/33.  
DR N-PSDB; AAS07061.  
XX  
PT New polypeptides derived from Streptococcus agalactiae are useful to  
PT provide detection of, and vaccination against, Group B Streptococcus  
PT infections, particularly to prevent infection in neonates.  
XX  
PS Claim 1; Fig 1; 178pp; English.  
XX  
CC AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus  
CC agalactiae) amino acid sequences of the invention. S. agalactiae is an  
CC encapsulated bacterium which is a major pathogen of humans causing sepsis  
CC and meningitis in neonates as well as adults. The S. agalactiae antigenic  
CC polypeptides are used to vaccinate against Group B Streptococcus  
CC infections, particularly to prevent infection in new born children  
CC arising from the maternal genital tract. An immunogenic composition is  
CC useful in the preparation of a medicament for the treatment or  
CC prophylaxis of Group B Streptococcus infection. The invention does not  
CC have the disadvantages of varied response rate associated with prior art  
CC capsid polysaccharide vaccination against Group B Streptococcus

XX SQ Sequence 452 AA;  
Query Match 89.5%; Score 34; DB 4; Length 452;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXKXW 7  
Db 92 GYWLSAW 98  
RESULT 4  
ABU21589  
ID ABU21589 standard; protein; 466 AA.  
XX AC ABU21589;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #7116.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Burkholderia fungorum.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX DR WPI; 2003-029926/02.  
DR N-PSDB; ACA25459.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 49513; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 466 AA;  
Query Match 89.5%; Score 34; DB 6; Length 466;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXKXW 7  
Db 86 GYWVSAW 92  
RESULT 5  
ABU38334  
ID ABU38334 standard; protein; 472 AA.  
XX AC ABU38334;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #23861.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Pseudomonas aeruginosa.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX DR WPI; 2003-029926/02.  
DR N-PSDB; ACA42204.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 66258; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of



CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 472 AA;

Query Match 89.5%; Score 34; DB 6; Length 472;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 94 GYWISAW 100

RESULT 6  
ABU24881  
ID ABU24881 standard; protein; 474 AA.  
XX  
AC ABU24881;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #10408.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Clostridium botulinum.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA28751.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 52805; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 474 AA;

Query Match 89.5%; Score 34; DB 6; Length 474;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 95 GYWLSAW 101

RESULT 7  
ABP30560  
ID ABP30560 standard; protein; 475 AA.  
XX  
AC ABP30560;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 10296.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus agalactiae.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB004789.  
XX  
PR 27-OCT-2000; 2000GB-00026333.  
PR 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-00005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Maignani V, Margarit Y Rosi, Grandi G, Fraser C;  
PI Tettelin H;



XX WPI; 2002-352536/38.  
DR N-PSDB; ABN71191.  
XX  
PT New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX  
PS Claim 1; Page 4161; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 475 AA;  
  
Query Match 89.5%; Score 34; DB 5; Length 475;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 92 GYWLSAW 98  
  
RESULT 8  
ABU40245  
ID ABU40245 standard; protein; 475 AA.  
XX  
AC ABU40245;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #25772.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Pseudomonas putida.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA44115.  
XX

PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 68169; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 475 AA;  
  
Query Match 89.5%; Score 34; DB 6; Length 475;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 93 GYWISAW 99  
  
RESULT 9  
ABU29756  
ID ABU29756 standard; protein; 475 AA.  
XX  
AC ABU29756;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #15283.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Enterococcus faecium.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA33626.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 57680; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 475 AA;  
  
Query Match 89.5%; Score 34; DB 6; Length 475;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 95 GYWLSAW 101  
  
RESULT 10  
ADC97241  
ID ADC97241 standard; protein; 478 AA.  
XX  
AC ADC97241;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE *E. faecium* protein sequence SEQ ID 6868.  
XX  
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;  
KW abdominal-pelvic infection.  
XX  
OS Enterococcus faecium.

XX US6583275-B1.  
PN  
XX 24-JUN-2003.  
PD  
XX 30-JUN-1998; 98US-00107532.  
PF  
XX 02-JUL-1997; 97US-0051571P.  
PR 14-MAY-1998; 98US-0085598P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-799836/75.  
DR N-PSDB; ADC93587.  
XX  
PT New isolated nucleic acid derived from *Enterococcus faecium* encoding an  
PT *Enterococcus faecium* polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.  
XX  
PS Example 1; SEQ ID NO 6868; 243pp; English.  
XX  
CC The invention relates to an isolated nucleic acid derived from  
CC *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcription regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids is useful for diagnosing pathological conditions  
CC resulting from *E. faecium* bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of *Candida albicans* -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating *Enterococcus faecium* infections. The present sequence represents  
CC one if the disclosed *E. faecium* proteins.  
XX  
SQ Sequence 478 AA;  
  
Query Match 89.5%; Score 34; DB 7; Length 478;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 98 GYWLSAW 104  
  
RESULT 11  
ABP26968  
ID ABP26968 standard; protein; 479 AA.  
XX  
AC ABP26968;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE *Streptococcus polypeptide* SEQ ID NO 3112.  
XX  
KW *Streptococcus*; GAS; GBS; group B *streptococcus*; *Streptococcus agalactiae*;  
KW group A *streptococcus*; *Streptococcus pyogenes*; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS *Streptococcus agalactiae*.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.  
PF  
XX 27-OCT-2000; 2000GB-00026333.  
PR  
PR 24-NOV-2000; 2000GB-00028727.  
PR  
XX 07-MAR-2001; 2001GB-00005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;  
PI Tettelin H;  
XX  
DR WPI; 2002-352536/38.  
DR N-PSDB; ABN67599.  
XX  
PT New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX  
PS Claim 1; Page 3464; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 479 AA;

Query Match 89.5%; Score 34; DB 5; Length 479;  
Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
Db 96 GYWLSAW 102

RESULT 12  
ABB55389  
ID ABB55389 standard; protein; 490 AA.  
XX  
AC ABB55389;  
XX  
DT 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX  
DE Lactococcus lactis protein arcD1.  
XX  
KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX  
OS Lactococcus lactis; IL1403.  
XX  
PN FR2807446-A1.  
XX  
PD 12-OCT-2001.  
XX  
PF ABB55389;  
XX  
DT 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX  
DE Lactococcus lactis protein arcD1.  
XX  
KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX  
OS Lactococcus lactis; IL1403.  
XX  
PN FR2807446-A1.  
XX  
PD 12-OCT-2001.  
XX  
PF 11-APR-2000; 2000FR-00004630.  
XX  
PR 11-APR-2000; 2000FR-00004630.

XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
PA Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
XX  
XX WPI; 2002-043418/06.  
DR  
XX  
PT New nucleotide sequence useful in the identification or Lactococcus  
PT lactis and related species.  
XX  
PS Claim 6; SEQ ID NO 2091; 2504pp; French.  
XX  
CC The present invention is related to a Lactococcus lactis nucleotide  
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
CC acid sequence is useful in the detection and/or amplification of nucleic  
CC acid sequence, particularly to identify Lactococcus lactis or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO200177334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 490 AA;

Query Match 89.5%; Score 34; DB 5; Length 490;  
Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
Db 93 GYWLSAW 99

RESULT 13  
ABB55385  
ID ABB55385 standard; protein; 496 AA.  
XX  
AC ABB55385;  
XX  
DT 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX  
DE Lactococcus lactis protein arcD2.  
XX  
KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX  
OS Lactococcus lactis; IL1403.  
XX  
PN FR2807446-A1.  
XX  
PD 12-OCT-2001.  
XX  
PF 11-APR-2000; 2000FR-00004630.  
XX  
PR 11-APR-2000; 2000FR-00004630.  
XX  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
XX  
PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
XX  
XX WPI; 2002-043418/06.  
DR  
XX  
PT New nucleotide sequence useful in the identification or Lactococcus  
PT lactis and related species.  
XX  
PS Claim 6; SEQ ID NO 2087; 2504pp; French.  
XX  
CC The present invention is related to a Lactococcus lactis nucleotide  
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
CC acid sequence is useful in the detection and/or amplification of nucleic



CC acid sequence, particularly to identify Lactococcus lactis or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO200177334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 496 AA;

Query Match 89.5%; Score 34; DB 5; Length 496;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
||| |  
Db 93 GYWISAW 99

RESULT 14  
ABO74582  
ID ABO74582 standard; protein; 499 AA.  
XX  
AC ABO74582;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #6757.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

DR WPI; 2003-615309/58.

DR N-PSDB; ABD08153.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 23328; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html

XX Sequence 499 AA;  
SQ Query Match 89.5%; Score 34; DB 7; Length 499;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
||| |  
Db 111 GYWISAW 117

RESULT 15  
ABU22414  
ID ABU22414 standard; protein; 506 AA.  
XX

AC ABU22414;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #7941.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia mallei.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA26284.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 50338; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 506 AA;

Query Match 89.5%; Score 34; DB 6; Length 506;  
Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
||| |  
Db 124 GYWISAW 130

Search completed: December 30, 2004, 13:07:56  
Job time : 51.7358 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 16.1132 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	478	4 US-09-107-532A-6868	Sequence 6868, Ap
2	34	89.5	499	4 US-09-252-991A-23328	Sequence 23328, A
3	34	89.5	865	4 US-09-252-991A-19339	Sequence 19339, A
4	33	86.8	543	4 US-09-252-991A-18697	Sequence 18697, A
5	33	86.8	1498	4 US-09-792-616-9	Sequence 9, Appli
6	33	86.8	1503	4 US-09-792-616-3	Sequence 3, Appli
7	32	84.2	177	4 US-09-543-681A-7620	Sequence 7620, Ap
8	32	84.2	252	3 US-09-502-653-10	Sequence 10, Appl
9	32	84.2	263	4 US-09-610-906-12	Sequence 12, Appl
10	32	84.2	274	4 US-09-248-796A-15791	Sequence 15791, A
11	32	84.2	278	4 US-09-145-828A-11	Sequence 11, Appl
12	32	84.2	278	4 US-09-903-456-18	Sequence 18, Appl
13	32	84.2	339	4 US-09-252-991A-26841	Sequence 26841, A
14	32	84.2	362	1 US-08-415-751-6	Sequence 6, Appli
15	32	84.2	367	4 US-09-248-796A-15188	Sequence 15188, A
16	32	84.2	492	4 US-09-107-532A-6945	Sequence 6945, Ap
17	32	84.2	500	4 US-09-252-991A-21214	Sequence 21214, A
18	31	81.6	342	4 US-09-252-991A-32031	Sequence 32031, A
19	30	78.9	11	4 US-09-069-827A-87	Sequence 87, Appl
20	30	78.9	16	4 US-09-620-091-81	Sequence 81, Appl
21	30	78.9	519	4 US-09-198-452A-479	Sequence 479, App
22	30	78.9	654	4 US-09-252-991A-18441	Sequence 18441, A
23	29	76.3	34	4 US-09-270-767-60715	Sequence 60715, A
24	29	76.3	35	3 US-09-082-279B-1191	Sequence 1191, Ap
25	29	76.3	35	3 US-09-315-304B-1191	Sequence 1191, Ap
26	29	76.3	35	4 US-09-834-784-1191	Sequence 1191, Ap
27	29	76.3	35	4 US-09-515-965A-1191	Sequence 1191, Ap

28	29	76.3	35	4 US-09-350-641C-1191	Sequence 1191, Ap
29	29	76.3	35	4 US-09-350-841A-1191	Sequence 1191, Ap
30	29	76.3	55	4 US-09-621-976-7633	Sequence 7633, Ap
31	29	76.3	69	4 US-09-621-976-7239	Sequence 7239, Ap
32	29	76.3	139	4 US-09-252-991A-19685	Sequence 19685, A
33	29	76.3	142	4 US-09-252-991A-23994	Sequence 22994, A
34	29	76.3	197	4 US-09-543-681A-5312	Sequence 5312, Ap
35	29	76.3	227	4 US-09-489-039A-8752	Sequence 8752, Ap
36	29	76.3	255	4 US-09-270-767-45223	Sequence 45223, A
37	29	76.3	625	4 US-09-252-991A-28537	Sequence 28537, A
38	29	76.3	930	4 US-09-198-452A-470	Sequence 470, App
39	28	73.7	19	4 US-09-794-529B-8	Sequence 8, Appli
40	28	73.7	19	4 US-09-794-517A-8	Sequence 8, Appli
41	28	73.7	19	4 US-09-011-645E-8	Sequence 8, Appli
42	28	73.7	19	4 US-09-794-832-8	Sequence 8, Appli
43	28	73.7	19	4 US-09-680-806A-8	Sequence 8, Appli
44	28	73.7	19	4 US-09-552-868-8	Sequence 8, Appli
45	28	73.7	19	4 US-09-636-295-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-107-532A-6868  
; Sequence 6868, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6868:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 478 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...478  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:  
US-09-107-532A-6868

Query Match 89.5%; Score 34; DB 4; Length 478;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
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Db 98 GYWLAW 104

RESULT 2  
US-09-252-991A-23328  
; Sequence 23328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23328  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23328

Query Match 89.5%; Score 34; DB 4; Length 499;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
| | | |  
Db 111 GYWISAW 117

RESULT 3  
US-09-252-991A-19339  
; Sequence 19339, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19339  
; LENGTH: 865  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19339

Query Match 89.5%; Score 34; DB 4; Length 865;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
| | | |  
Db 487 GYWISAW 493

RESULT 4

US-09-252-991A-18697  
; Sequence 18697, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18697  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18697

Query Match 86.8%; Score 33; DB 4; Length 543;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
| | | |  
Db 331 GYWMVSW 337

RESULT 5  
US-09-792-616-9  
; Sequence 9, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-792-616-9

Query Match 86.8%; Score 33; DB 4; Length 1498;  
Best Local Similarity 57.1%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
| | | |  
Db 960 GYWLWLW 966

RESULT 6  
US-09-792-616-3  
; Sequence 3, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      86.8%; Score 33; DB 4; Length 1503;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      965 GYWLSLW 971

RESULT 7
US-09-543-681A-7620
; Sequence 7620, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7620
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7620

Query Match      84.2%; Score 32; DB 4; Length 177;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      43 GYVWINW 49

RESULT 8
US-09-502-653-10
; Sequence 10, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schlein, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481.200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Bacillus circulans
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US-09-502-653-10

Query Match      84.2%; Score 32; DB 3; Length 252;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      210 GYWEPAW 216

RESULT 9
US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Klinger, Tod M.
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT
; FILE REFERENCE: PC-0012 CIP
; CURRENT APPLICATION NUMBER: US/09/610,906
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 09/226,994
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. 6566066: g2346968
; PUBLICATION INFORMATION:
US-09-610-906-12

Query Match      84.2%; Score 32; DB 4; Length 263;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      224 GYWDFHW 230

RESULT 10
US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15791
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791

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Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      84 GYWPITW 90
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RESULT 11
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      84.2%; Score 32; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
||| |
Db      108 GYWIFLW 114

RESULT 12
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match      84.2%; Score 32; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
||| |
Db      108 GYWIFLW 114
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RESULT 13
US-09-252-991A-26841
; Sequence 26841, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26841
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26841

Query Match      84.2%; Score 32; DB 4; Length 339;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      261 GYWGgyW 267

RESULT 14
US-08-415-751-6
; Sequence 6, Application US/08415751
; Patent No. 5643772
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-
; TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, DNA
; TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID
; TITLE OF INVENTION: VECTOR AND TRANSFORMED HOST AND
; TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS AND KIT
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILLIPS, MOORE, LEMPPIO & FINLEY
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,751
; FILING DATE: 03-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/071,880
; FILING DATE: June 1, 1993
; APPLICATION NUMBER: 07/891,301
; FILING DATE: May 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana Dolezalova
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-1677  
TELEFAX: (415) 324-1678  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 362 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Cryptosporidium parvum  
FEATURE:  
NAME/KEY: Positions coded by nonsense codons are  
NAME/KEY: identified as xaa.  
US-08-415-751-6

Query Match 84.2%; Score 32; DB 1; Length 362;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
Db 216 GYWLTW 222

RESULT 15  
US-09-248-796A-15188  
; Sequence 15188, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 15188  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-15188

Query Match 84.2%; Score 32; DB 4; Length 367;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
Db 276 GYWLVDW 282

Search completed: December 30, 2004, 13:19:22  
Job time : 18.1132 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 13:08:04 ; Search time 52.1698 Seconds  
(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
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13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	58	17	US-10-425-115-308836 Sequence 308836,
2	34	89.5	72	16	US-10-437-963-176036 Sequence 176036,
3	34	89.5	452	14	US-10-091-007-88 Sequence 88, Appl
4	34	89.5	466	15	US-10-282-122A-49513 Sequence 49513, A
5	34	89.5	469	14	US-10-369-493-23291 Sequence 23291, A
6	34	89.5	472	15	US-10-282-122A-66258 Sequence 66258, A
7	34	89.5	474	15	US-10-282-122A-52805 Sequence 52805, A
8	34	89.5	475	14	US-10-369-493-13733 Sequence 13733, A
9	34	89.5	475	15	US-10-282-122A-57680 Sequence 57680, A
10	34	89.5	475	15	US-10-282-122A-68169 Sequence 68169, A
11	34	89.5	506	15	US-10-282-122A-50338 Sequence 50338, A
12	34	89.5	585	9	US-09-894-018-87 Sequence 87, Appl
13	34	89.5	585	17	US-10-474-960A-87 Sequence 87, Appl

14	33	86.8	10	13	US-10-046-922-34	Sequence 34, Appl
15	33	86.8	10	13	US-10-046-922-35	Sequence 35, Appl
16	33	86.8	47	17	US-10-425-115-287762	Sequence 287762,
17	33	86.8	104	17	US-10-425-115-273234	Sequence 273234,
18	33	86.8	116	10	US-09-910-483-1	Sequence 1, Appli
19	33	86.8	116	10	US-09-910-483-5	Sequence 5, Appli
20	33	86.8	116	10	US-09-910-483-9	Sequence 9, Appli
21	33	86.8	116	10	US-09-910-483-13	Sequence 13, Appl
22	33	86.8	116	10	US-09-910-483-17	Sequence 17, Appl
23	33	86.8	116	10	US-09-910-483-21	Sequence 21, Appl
24	33	86.8	116	10	US-09-910-483-25	Sequence 25, Appl
25	33	86.8	116	10	US-09-910-483-29	Sequence 29, Appl
26	33	86.8	116	10	US-09-910-483-33	Sequence 33, Appl
27	33	86.8	116	10	US-09-910-483-37	Sequence 37, Appl
28	33	86.8	116	10	US-09-910-483-41	Sequence 41, Appl
29	33	86.8	116	10	US-09-910-483-43	Sequence 43, Appl
30	33	86.8	129	17	US-10-425-115-357518	Sequence 357518,
31	33	86.8	138	14	US-10-160-232-86	Sequence 86, Appl
32	33	86.8	138	14	US-10-160-232-90	Sequence 90, Appl
33	33	86.8	227	15	US-10-282-122A-64263	Sequence 64263, A
34	33	86.8	229	17	US-10-425-115-344695	Sequence 344695,
35	33	86.8	296	14	US-10-156-761-9632	Sequence 9632, Ap
36	33	86.8	296	14	US-10-369-493-19811	Sequence 19811, A
37	33	86.8	466	14	US-10-369-493-16537	Sequence 16537, A
38	33	86.8	467	16	US-10-437-963-199114	Sequence 199114,
39	33	86.8	516	16	US-10-450-022-7	Sequence 7, Appli
40	33	86.8	526	16	US-10-450-022-4	Sequence 4, Appli
41	33	86.8	526	16	US-10-450-022-5	Sequence 5, Appli
42	33	86.8	526	17	US-10-433-747B-2	Sequence 2, Appli
43	33	86.8	526	17	US-10-433-747B-17	Sequence 17, Appl
44	33	86.8	526	17	US-10-450-185B-2	Sequence 2, Appli
45	33	86.8	526	17	US-10-450-185B-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-425-115-308836  
; Sequence 308836, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 308836  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_44726C.1.pep  
; US-10-425-115-308836

Query Match 89.5%; Score 34; DB 17; Length 58;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
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Db 49 GYWGASW 55

RESULT 2

US-10-437-963-176036  
; Sequence 176036, Application US/10437963  
; Publication No. US20040123343A1

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; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176036
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
US-10-437-963-176036

Query Match      89.5%; Score 34; DB 16; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      34 GYWSSHW 40

RESULT 3
US-10-091-007-88
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited
; APPLICANT: Le Page, Richard W F Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88

Query Match      89.5%; Score 34; DB 14; Length 452;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      92 GYWLSAW 98

RESULT 4
US-10-282-122A-49513
; Sequence 49513, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
```

```
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49513
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49513

Query Match      89.5%; Score 34; DB 15; Length 466;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      86 GYWWSAW 92

RESULT 5
US-10-369-493-23291
; Sequence 23291, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23291
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Query Match 89.5%; Score 34; DB 14; Length 469;  
Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
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Db 97 GYWVASW 103

RESULT 6

US-10-282-122A-66258  
; Sequence 66258, Application US/10282122A  
; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66258  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-66258  
; GENERAL INFORMATION:

Query Match 89.5%; Score 34; DB 15; Length 472;  
Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
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Db 94 GYWISAW 100

RESULT 7

US-10-282-122A-52805  
; Sequence 52805, Application US/10282122A  
; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52805  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Clostridium botulinum

US-10-282-122A-52805

Query Match 89.5%; Score 34; DB 15; Length 474;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
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Db 95 GYWLSAW 101

RESULT 8

US-10-369-493-13733  
; Sequence 13733, Application US/10369493  
; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 13733



; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Pseudomonas fluorescens  
US-10-369-493-13733

Query Match 89.5%; Score 34; DB 14; Length 475;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
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Db 93 GYWISAW 99

RESULT 9

US-10-282-122A-57680  
; Sequence 57680, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 57680

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Enterococcus faecium

US-10-282-122A-57680

Query Match 89.5%; Score 34; DB 15; Length 475;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
||| |  
Db 95 GYWLSAW 101

RESULT 10

US-10-282-122A-68169  
; Sequence 68169, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 68169

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Pseudomonas putida

US-10-282-122A-68169

Query Match 89.5%; Score 34; DB 15; Length 475;

Best Local Similarity 57.1%; Pred. No. 5.9e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7  
||| |  
Db 93 GYWISAW 99

RESULT 11

US-10-282-122A-50338  
; Sequence 50338, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 50338  
; LENGTH: 506  
; TYPE: PRT  
; ORGANISM: Burkholderia mallei  
US-10-282-122A-50338

Query Match 89.5%; Score 34; DB 15; Length 506;  
Best Local Similarity 57.1%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 124 GYWISAW 130

RESULT 12  
US-09-894-018-87  
; Sequence 87, Application US/09894018  
; Patent No. US20020119127A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Deniaw  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY  
; FILE REFERENCE: 39963-20033.00  
; CURRENT APPLICATION NUMBER: US/09/894,018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: PCT/US00/35568  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 87  
; LENGTH: 585  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV-TC  
US-09-894-018-87

Query Match 89.5%; Score 34; DB 9; Length 585;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 22 GYWQATW 28

RESULT 13  
US-10-474-960A-87  
; Sequence 87, Application US/10474960A  
; Publication No. US20040248113A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Denise  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic  
; TITLE OF INVENTION: Acid Constructs and Peptides Encoded Thereby  
; FILE REFERENCE: 2060.0320004  
; CURRENT APPLICATION NUMBER: US/10/474,960A  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: PCT/US02/09877  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 09/894,018  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 87  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV-TC  
US-10-474-960A-87

Query Match 89.5%; Score 34; DB 17; Length 585;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 22 GYWQATW 28

RESULT 14  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide

; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 86.8%; Score 33; DB 13; Length 10;  
Best Local Similarity 57.1%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 2 GYWLTIW 8

RESULT 15  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
US-10-046-922-35

Query Match 86.8%; Score 33; DB 13; Length 10;  
Best Local Similarity 57.1%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 2 GYWLTIW 8

Search completed: December 30, 2004, 13:50:02  
Job time : 53.1698 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 8.0566 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	72	2 T03190	hypothetical prote
2	34	89.5	108	2 S12193	hypothetical prote
3	34	89.5	345	2 T37139	hypothetical prote
4	34	89.5	469	2 D70048	ABC transporter (a
5	34	89.5	472	2 E83497	probable amino aci
6	34	89.5	475	2 T46745	arginine/ornithine
7	34	89.5	482	2 JH0110	arginine/ornithine
8	34	89.5	490	2 C86879	arginine/ornitine
9	34	89.5	497	2 G86878	arginine/ornitine
10	33	86.8	142	2 C34903	Ig heavy chain pre
11	33	86.8	227	2 S73905	CDPdiacylglycerol-
12	33	86.8	250	2 A69843	hypothetical prote
13	33	86.8	289	2 G72215	oligopeptide ABC t
14	33	86.8	360	2 AE2047	hypothetical prote
15	33	86.8	441	2 C95307	probable transport
16	33	86.8	508	2 C95282	probable ABC trans
17	33	86.8	517	2 AI3201	hypothetical prote
18	33	86.8	519	2 E83268	probable carbohydr
19	33	86.8	534	2 T15414	hypothetical prote
20	33	86.8	535	2 B95952	probable dipeptide
21	33	86.8	541	2 AC2392	hypothetical prote
22	33	86.8	563	2 AH2975	hypothetical prote
23	33	86.8	563	2 C98307	opHA protein limpo
24	33	86.8	592	2 T15413	hypothetical prote
25	33	86.8	778	2 T31037	hypothetical prote
26	33	86.8	1502	2 T42216	multidrug resistan
27	32	84.2	71	2 S22905	lysis protein S -
28	32	84.2	83	2 E69903	hypothetical prote
29	32	84.2	187	2 G83047	hypothetical prote

ALIGNMENTS

RESULT 1

T03190

hypothetical protein 72B - rice mitochondrion  
C;Species: mitochondrion Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

C;Accession: T03190

R;Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.

Plant Cell Physiol. 35, 1239-1244, 1994

A;Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existence

A;Reference number: Z14841; MUID:95211382; PMID:7545979

A;Accession: T03190

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA

A;Residues: 1-72 <ITA>

A;Cross-references: UNIPROT:Q35302; EMBL:D32052; NID:g769704; PIDN:BAA06811.1; PID:g76970

A;Experimental source: cultivar Nipponbare

C;Genetics:

A;Genome: mitochondrion

C;Keywords: mitochondrion

Query Match 89.5%; Score 34; DB 2; Length 72;  
Best Local Similarity 57.1%; Pred. No. 15;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
|||  
Db 34 GYWSSHW 40

RESULT 2

S12193

hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1

C;Species: Thiobacillus ferrooxidans

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S12193

R;Drolet, M.; Zanga, P.; Lau, P.C.K.

Mol. Microbiol. 4, 1381-1391, 1990

A;Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans f

A;Reference number: S12188; MUID:91125140; PMID:2280689

A;Accession: S12193

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-108 <DRO>

A;Cross-references: UNIPROT:P20088; EMBL:X52699; NID:g48158; PIDN:CAA36930.1; PID:g48164

C;Genetics:

A;Genome: plasmid pTF1

Query Match 89.5%; Score 34; DB 2; Length 108;  
Best Local Similarity 57.1%; Pred. No. 21;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

Db89 GYWRSSW 95

RESULT 3

T37139

hypothetical protein SCJ9A.03c - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T37139

R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999

A;Reference number: Z21622

A;Accession: T37139

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-345 <HAR>

A;Cross-references: UNIPROT:Q9S1R7; EMBL:AL109972; PIDN:CAB53264.1; GSPDB:GN00070; SCOE

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SCJ9A.03c

C;Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c

Query Match89.5%; Score 34; DB 2; Length 345;

Best Local Similarity57.1%; Pred. No. 61;

Matches4; Conservative0; Mismatches3; Indels0; Gaps0;

Qy1 GYWXXXW 7

Db147 GYWAARW 153

RESULT 4

D70048

ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C;Accession: D70048

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: D70048

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <KUN>

A;Cross-references: UNIPROT:O32204; GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15339.

A;Experimental source: strain 168

C;Genetics:

A;Gene: yvsh

C;Superfamily: L-lysine transport protein

Query Match89.5%; Score 34; DB 2; Length 469;

Best Local Similarity57.1%; Pred. No. 80;

Matches4; Conservative0; Mismatches3; Indels0; Gaps0;

Qy1 GYWXXXW 7

Db97 GYVVASW 103

RESULT 5		
E83497	probable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PAO1)	
C;Species:	Pseudomonas aeruginosa	
C;Date:	15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004	
C;Accession:	E83497	
R;Stover, C.K.;	Pham, X.Q.;	Erwin, A.L.;
Mizoguchi, S.D.;	Warrener, P.;	Hickey, M.J.;
Br adman, S.;	Yuan, Y.;	Brody, L.L.;
Coulter, S.N.;	Folger, K.R.;	Kas, A.;
Larbig, K.;	Lim, .;	Lory, S.;
Olson, M.V. Nature 406, 959-964, 2000		
A;Title:	Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen	
A;Reference number:	A82950;	MUID:20437337;
PMID:10984043		
A;Accession:	E83497	
A;Status:	preliminary	
A;Molecule type:	DNA	
A;Residues:	1-472 <STO>	
A;Cross-references:	UNIPROT:Q9I4E4;	GB:AE004549;
GB:AE004091;	NID:g9947110;	PIDN:AAG0458.
A;Experimental source:	strain PAO1	
C;Genetics:		
A;Gene:	PA1194	
C;Superfamily:	L-lysine transport protein	
Query Match	89.5%;	Score 34; DB 2; Length 472;
Best Local Similarity	57.1%;	Pred. No. 81;
Matches	4; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7	
Db	94 GYWISAW 100	
RESULT 6		
T46745	arginine/ornithine antiporter [imported] - Lactobacillus sakei	
C;Species:	Lactobacillus sakei	
C;Date:	20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004	
C;Accession:	T46745	
R;Zuniga, M.;	Championier-Verges, M.C.;	Perez-Martinez, G.;
Zagorec, M.;	Perez-Martinez, C. J. Bacteriol. 180, 4154-4159, 1998	
A;Title:	Structural and functional analysis of the gene cluster encoding the enzymes of the arginine/ornithine antiporter	
A;Reference number:	Z23141;	MUID:98361904;
PMID:9696763		
A;Accession:	T46745	
A;Status:	preliminary;	translated from GB/EMBL/DDBJ
A;Molecule type:	DNA	
A;Residues:	1-475 <ZUN>	
A;Cross-references:	UNIPROT:O53092;	EMBL:AJ001330;
NID:g2764610;	PIDN:CAA04686.1;	PID:g2. C;Genetics:
A;Gene:	arcD	
C;Function:		
A;Description:	necessary for arginine transport; involved in ornithine-arginine exchange	
A;Pathway:	arginine catabolism	
C;Superfamily:	L-lysine transport protein	
Query Match	89.5%;	Score 34; DB 2; Length 475;
Best Local Similarity	57.1%;	Pred. No. 81;
Matches	4; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7	
Db	94 GYWLSAW 100	
RESULT 7		
JH0110	arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa	
C;Species:	Pseudomonas aeruginosa	
C;Date:	31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004	
C;Accession:	JH0110;	A82999
R;Luethi, E.;	Baur, H.;	Gamper, M.;
Brunner, F.;	Villeva, D.;	Mercenier, A.;
Haas, D. Gene 87, 37-43, 1990		
A;Title:	The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cont	
A;Reference number:	JH0110;	MUID:90236296;
PMID:2158926		
A;Accession:	JH0110	



A;Molecule type: DNA  
A;Residues: 1-482 <LUE>  
A;Cross-references: UNIPROT:P18275; GB:M33223; NID:g151030; PIDN:AA25719.1; PID:g151031  
A;Experimental source: strain PA01  
A;Note: the gene encoding this protein is located upstream of the arcABC genes which encode for the synthesis of L-lysine  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: A82999  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-482 <STO>  
A;Cross-references: GB:AE004930; GB:AE004091; NID:g9951472; PIDN:AAG08555.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: arcD; PA5170  
C;Superfamily: L-lysine transport protein  
C;Keywords: transmembrane protein  
  
Query Match 89.5%; Score 34; DB 2; Length 482;  
Best Local Similarity 57.1%; Pred. No. 82;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 94 GYWISAW 100  
  
RESULT 8  
C86879  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: C86879  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: C86879  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-490 <STO>  
A;Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:G12725084  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: arcD1  
C;Superfamily: L-lysine transport protein  
  
Query Match 89.5%; Score 34; DB 2; Length 490;  
Best Local Similarity 57.1%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 93 GYWLAW 99  
  
RESULT 9  
G86878  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: G86878  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: G86878  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-497 <STO>  
A;Cross-references: UNIPROT:Q9CE19; GB:AE005176; PID:g12725079; PIDN:AAK06129.1; GSPDB:G12725079  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: arcD2  
C;Superfamily: L-lysine transport protein  
  
Query Match 89.5%; Score 34; DB 2; Length 497;  
Best Local Similarity 57.1%; Pred. No. 85;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 93 GYWISAW 99  
  
RESULT 10  
C34903  
Ig heavy chain precursor V region (5-27) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
C;Accession: C34903  
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive antibodies  
A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: C34903  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-142 <BED>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-119/Domain: immunoglobulin homology <IMM>  
  
Query Match 86.8%; Score 33; DB 2; Length 142;  
Best Local Similarity 57.1%; Pred. No. 40;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 126 GYWFAYW 132  
  
RESULT 11  
S73905  
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) pgsA - Mycobacterium tuberculosis  
N;Alternate names: hypothetical protein A65\_orf227  
C;Species: Mycoplasma pneumoniae  
A;Variety: ATCC 29342  
C;Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S73905  
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
A;Reference number: S73327; MUID:97105885; PMID:8948633  
A;Accession: S73905  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-227 <HIM>  
A;Cross-references: UNIPROT:P75520; EMBL:AE000057; GB:U00089; NID:g1674279; PIDN:AAB9622.1  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C;Genetics:  
A;Gene: pgsA  
A;Genetic code: SGC3  
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase  
C;Keywords: transferase  
  
Query Match 86.8%; Score 33; DB 2; Length 227;  
Best Local Similarity 57.1%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |

Db	84 GYWARQW 90
RESULT 12	
A69843	hypothetical protein yjba - Bacillus subtilis
C;Species: Bacillus subtilis	
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004	
C;Accession: A69843	
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton	
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho	
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.	
Nature 390, 249-256, 1997	
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler	
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.	
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,	
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel	
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle	
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,	
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron	
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,	
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K	
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.	
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.	
A;Reference number: A69580; MUID:98044033; PMID:9384377	
A;Accession: A69843	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA	
A;Residues: 1-250 <KUN>	
A;Cross-references: UNIPROT:O31597; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB12998.	
A;Experimental source: strain 168	
C;Genetics:	
A;Gene: yjba	
C;Superfamily: Bacillus subtilis hypothetical protein yjba	
Query Match	86.8%; Score 33; DB 2; Length 250;
Best Local Similarity	57.1%; Pred. No. 68;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7
Db	185 GYWYTEW 191
RESULT 13	
G72215	oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima	
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004	
C;Accession: G72215	
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey	
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;	
C.M.	
Nature 399, 323-329, 1999	
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq	
A;Reference number: A72200; MUID:99287316; PMID:10360571	
A;Accession: G72215	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-289 <ARN>	
A;Cross-references: UNIPROT:Q9X270; GB:AE001813; GB:AE000512; NID:g4982321; PIDN:AAD3681	
A;Experimental source: strain MSB8	
C;Genetics:	
A;Gene: TM1748	
C;Superfamily: oligopeptide permease protein oppB	
Query Match	86.8%; Score 33; DB 2; Length 289;
Best Local Similarity	57.1%; Pred. No. 77;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7
Db	11 GYWKAFW 17

RESULT 14

AE2047	hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120	
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120	
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004	
C;Accession: AE2047	
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,	
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S	
DNA Res. 8, 205-213, 2001	
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal	
A;Reference number: AB1807; MUID:21595285; PMID:11759840	
A;Accession: AE2047	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-360 <KUR>	
A;Cross-references: UNIPROT:Q8YVP3; GB:BA000019; PIDN:BA073630.1; PID:gl7131021; GSPDB:G	
A;Experimental source: strain PCC 7120	
C;Genetics:	
A;Gene: all1931	
Query Match	86.8%; Score 33; DB 2; Length 360;
Best Local Similarity	57.1%; Pred. No. 94;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7
Db	127 GYWSYGW 133
RESULT 15	
C95307	probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) mag
C;Species: Sinorhizobium meliloti	
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004	
C;Accession: C95307	
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows	
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.	
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001	
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti	
A;Reference number: A95262; MUID:21396509; PMID:11481432	
A;Accession: C95307	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-441 <KUR>	
A;Cross-references: UNIPROT:Q92ZT6; GB:AB006469; PIDN:AAK65021.1; PID:gl4523451; GSPDB:G	
A;Experimental source: strain 1021, megaplasmid pSymA	
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,	
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;	
L.; Hyman, R.W.; Jones, T.	
Science 293, 668-672, 2001	
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,	
hebaült, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.	
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.	
A;Reference number: A96039; MUID:21368234; PMID:11474104	
A;Contents: annotation	
C;Genetics:	
A;Gene: Sma0684	
A;Genome: plasmid	
C;Superfamily: L-lysine transport protein	
Query Match	86.8%; Score 33; DB 2; Length 441;
Best Local Similarity	57.1%; Pred. No. 1.1e+02;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7
Db	92 GYWISIW 98

Job time : 10.2233 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 64.5849 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	72	2 Q35302	Q35302 oryza sativ
2	34	89.5	108	1 YML2 THIFE	P20088 thicobacillu
3	34	89.5	130	2 Q7U395	Q7u395 prochloroco
4	34	89.5	236	2 Q9WGW9	Q9wgw9 human immun
5	34	89.5	253	2 Q32816	Q32816 lactococcus
6	34	89.5	294	2 Q8ET30	Q8et30 oceanobacil
7	34	89.5	333	2 Q6F6U4	Q6f6u4 acinetobact
8	34	89.5	345	2 Q9SLR7	Q9slr7 streptomyce
9	34	89.5	459	2 Q9KGV3	Q9kgv3 lactococcus
10	34	89.5	464	2 Q84DL5	Q84dl5 oenococcus
11	34	89.5	465	2 Q6HNI4	Q6hni4 bacillus th
12	34	89.5	465	2 Q6I3F7	Q6i3f7 bacillus an
13	34	89.5	465	2 Q73DL5	Q73dl5 bacillus ce
14	34	89.5	465	2 Q8IHZ7	Q8ihz7 bacillus ce
15	34	89.5	465	2 Q81V71	Q81v71 bacillus an
16	34	89.5	465	2 AAS39630	Aas39630 bacillus
17	34	89.5	465	2 AAT29732	Aat29732 bacillus
18	34	89.5	469	2 Q6TK71	Q6tk71 streptococc
19	34	89.5	469	2 Q32204	Q32204 bacillus su
20	34	89.5	469	2 AAR30325	Aar30325 streptoco
21	34	89.5	471	2 Q6HP27	Q6hp27 bacillus th
22	34	89.5	471	2 Q73E85	Q73e85 bacillus ce
23	34	89.5	471	2 Q81IH9	Q81ih9 bacillus ce
24	34	89.5	471	2 AAS39409	Aas39409 bacillus
25	34	89.5	472	2 Q914E4	Q9i4e4 pseudomonas
26	34	89.5	473	2 Q7NRJ8	Q7nrj8 chromobacte
27	34	89.5	475	1 ARCD_LACSK	O53092 lactobacill
28	34	89.5	475	2 Q88P50	Q88p50 pseudomonas
29	34	89.5	475	2 Q88P51	Q88p51 pseudomonas
30	34	89.5	475	2 Q8DWP9	Q8dwp9 streptococc
31	34	89.5	475	2 Q8E2J7	Q8e2j7 streptococc

32	34	89.5	478	1 ARCD_CLOPE	Q46170 clostridium
33	34	89.5	482	1 ARCD_PSEAE	P18275 pseudomonas
34	34	89.5	490	2 Q9CEI5	Q9cel5 lactococcus
35	34	89.5	497	2 Q9KGV0	Q9kgv0 lactococcus
36	34	89.5	497	2 Q9CE19	Q9cel9 lactococcus
37	34	89.5	526	2 Q9K574	Q9k574 lactococcus
38	34	89.5	879	2 Q7ZJJ7	Q7zjj7 human immun
39	33	86.8	130	2 Q7VBG3	Q7vbg3 prochloroco
40	33	86.8	135	2 Q7TUV7	Q7tuv7 prochloroco
41	33	86.8	160	2 Q6NF17	Q6nf17 corynebacte
42	33	86.8	160	2 CAE50615	Caes0615 corynebac
43	33	86.8	213	2 Q9KY37	Q9ky37 streptomyc
44	33	86.8	224	2 Q8S486	Q8s486 zea mays (m
45	33	86.8	227	1 PGSA_MYCPN	P75520 mycoplasma

ALIGNMENTS

RESULT 1  
Q35302 ID Q35302 PRELIMINARY; PRT; 72 AA.  
AC Q35302;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
DE ORF72B.

OS Oryza sativa (japonica cultivar-group).  
OG Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Baev A.A., Dzhumagaliy E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,  
RA Il'in Y.V.;  
RT "Structure of long and short copies of the mobile dispersed gene MDG3  
of Drosophila melanogaster.";  
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95308541; PubMed=7788722;  
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiyura M.,  
RA Hirai A.;  
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is  
transcribed from alternative promoters.";  
RL Curr. Genet. 27:184-189(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95211382; PubMed=7545979;  
RA Itadani H., Wakasugi T., Sugita M., Sugiyura M., Nakazono M., Hirai A.;  
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:  
the existence of many sequences that correspond to parts of  
mitochondrial genes in intergenic regions.";  
RL Plant Cell Physiol. 35:1239-1244(1994).  
DR EMBL; D32052; BAA06811.1; -.  
DR PIR; T03190; T03190.  
DR Gramene; Q35302; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
SQ SEQUENCE 72 AA; 8155 MW; D42DE53BED28432E CRC64;

Query Match 89.5%; Score 34; DB 2; Length 72;  
Best Local Similarity 57.1%; Pred. No. 87;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

Db 34 GYWSSHW 40

RESULT 2



YML2\_THIFE  
ID YML2\_THIFE STANDARD; PRT; 108 AA.  
AC P20088;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 12.3 kDa protein in mobL 3'region (ORF 4).  
OS Thiobacillus ferrooxidans.  
OG Plasmid pTF1.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;  
OC Acidithiobacillaceae; Acidithiobacillus.  
OX NCBI\_TaxID=920;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33020;  
RX MEDLINE=91125140; PubMed=2280689;  
RA Drolet M., Zanga P., Lau P.C.K.;  
RT "The mobilization and origin of transfer regions of a Thiobacillus  
RT ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";  
RL Mol. Microbiol. 4:1381-1391(1990).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X52699; CAA36930.1; -.  
DR PIR; S12193; S12193.  
KW Hypothetical protein; Plasmid.  
SQ SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;  
  
Query Match 89.5%; Score 34; DB 1; Length 108;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 89 GYWRSSW 95  
  
RESULT 3  
Q7U395 PRELIMINARY; PRT; 130 AA.  
ID Q7U395  
AC Q7U395;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Possible Adenoviral fiber protein (Repeat/shaf.  
GN OrderedLocusNames=PMW1067;  
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).  
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=59919;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;  
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,  
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,  
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,  
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,  
RA Webb E.A., Zinser E.R., Chisholm S.W.;  
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic  
RT niche differentiation."  
RL Nature 424:1042-1047(2003).  
DR EMBL; BX572092; CAE19526.1; -.  
KW Complete proteome.  
SQ SEQUENCE 130 AA; 14024 MW; EE0F4A997FCA8CD8 CRC64;  
  
Query Match 89.5%; Score 34; DB 2; Length 130;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 7 GYWT LAW 13  
  
RESULT 4  
Q9WGW9 PRELIMINARY; PRT; 236 AA.  
ID Q9WGW9  
AC Q9WGW9;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Polyprotein (Fragment).  
GN Name=pol;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99214336; PubMed=10196293;  
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,  
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,  
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,  
RA Walker B.D.;  
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition  
RT in perinatal human immunodeficiency virus (HIV) type 1 transmission:  
RT the ariel project for the prevention of transmission of HIV from  
RT mother to infant."  
RL J. Virol. 73:3975-3985(1999).  
DR EMBL; AF121641; AAD29013.1; -.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0004523; F:ribonuclease H activity; IEA.  
DR InterPro; IPR002156; RNaseH.  
DR InterPro; IPR010659; RVT\_connect.  
DR InterPro; IPR010661; RVT\_thumb.  
DR Pfam; PF00075; RNaseH; 1.  
DR Pfam; PF06815; RVT\_connect; 1.  
DR Pfam; PF06817; RVT\_thumb; 1.  
KW Polyprotein.  
FT NON\_TER 1 1  
FT NON\_TER 236 236  
SQ SEQUENCE 236 AA; 27062 MW; 24D6BB0409A80BB8 CRC64;  
  
Query Match 89.5%; Score 34; DB 2; Length 236;  
Best Local Similarity 57.1%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
||| |  
Db 129 GYWQATW 135  
  
RESULT 5  
O32816 PRELIMINARY; PRT; 253 AA.  
ID O32816  
AC O32816;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Arginine/ornithine antiporter homolog ArcD (Fragment).  
GN Name=arcD;  
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MG1363;  
RX MEDLINE=97369814; PubMed=9226255;  
RA Duwat P., Cochu A., Ehrlich S.D., Gruss A.;  
RT "Characterization of Lactococcus lactis UV-sensitive mutants obtained  
RT by ISS1 transposition.";

RL J. Bacteriol. 179:4473-4479(1997).  
DR EMBL; U81991; AAC45504.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permease1.  
KW Transmembrane.  
FT NON TER 253 253  
SQ SEQUENCE 253 AA; 26569 MW; 1CB8FAEF6C38FBB1 CRC64;  
  
Query Match 89.5%; Score 34; DB 2; Length 253;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
Db 93 GYWLAW 99  
  
RESULT 6  
Q8ET30 PRELIMINARY; PRT; 294 AA.  
ID Q8ET30  
AC Q8ET30;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ABC transporter permease.  
GN OrderedLocusNames=OB0434;  
OS Oceanobacillus iheyensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831;  
RX MEDLINE=22220767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments.";  
RL Nucleic Acids Res. 30:3927-3935(2002).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE ABC-3 SUBFAMILY OF INTEGRAL MEMBRANE  
CC PROTEINS.  
DR EMBL; AP004594; BAC12390.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001626; ABC\_3.  
DR Pfam; PF00950; ABC-3; 1.  
KW Complete proteome; Transmembrane; Transport.  
SQ SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;  
  
Query Match 89.5%; Score 34; DB 2; Length 294;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
Db 244 GYWIATW 250  
  
RESULT 7  
Q6F6U4 PRELIMINARY; PRT; 333 AA.  
ID Q6F6U4  
AC Q6F6U4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Putative transporter; putative sodium/bile acid transporter family  
DE protein.  
GN OrderedLocusNames=ACIAD3583;  
OS Acinetobacter sp. (strain ADP1).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=62977;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,  
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,  
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;  
RT "Unique features revealed by the genome sequence of Acinetobacter sp.  
RT ADP1, a versatile and naturally transformation competent bacterium.";  
RL Nucleic Acids Res. 0:0-0(2004).  
DR EMBL; CR543861; CAG70223.1; -.  
DR InterPro; IPR002657; BilAc/Na\_sympoort.  
DR Pfam; PF01758; SBF; 1.  
KW Complete proteome.  
SQ SEQUENCE 333 AA; 36530 MW; 7C887F5127A40682 CRC64;  
  
Query Match 89.5%; Score 34; DB 2; Length 333;  
Best Local Similarity 57.1%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
Db 252 GYWASRW 258  
  
RESULT 8  
Q9S1R7 PRELIMINARY; PRT; 345 AA.  
ID Q9S1R7  
AC Q9S1R7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein SCO0224.  
GN OrderedLocusNames=SCO0224; ORFNames=SCJ9A.03C;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL939104; CAB53264.1; -.  
DR PIR; T37139; T37139.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;  
  
Query Match 89.5%; Score 34; DB 2; Length 345;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
Db 147 GYWAARW 153  
  
RESULT 9  
Q9KGV3 PRELIMINARY; PRT; 459 AA.  
ID Q9KGV3  
AC Q9KGV3;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ArcD1.  
GN Name=arcD1;  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1360;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML3;  
RA Chou L., Weimer B., Xie Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML3;  
RA Chou L.-S., Weimer B., Xie Y.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF282249; AAF86987.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 459 AA; 49146 MW; 9718F27B7E937242 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 459;  
Best Local Similarity 57.1%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 92 GYWLSAW 98

RESULT 10  
Q84DL5 PRELIMINARY; PRT; 464 AA.  
AC Q84DL5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Arginine/ornithine antiporter ArcD2.  
GN Name=arcD2;  
OS Oenococcus oeni (Leuconostoc oenos).  
OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.  
OX NCBI\_TaxID=1247;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 23279;  
RX MEDLINE=22519090; PubMed=12631210;  
RA Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;  
RT "Molecular characterization of Oenococcus oeni genes encoding proteins  
involved in arginine transport.";  
RL J. Appl. Microbiol. 94:738-746 (2003).  
RE EMBL; AF541253; AA083382.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 464 AA; 50557 MW; 1C6EE79AFF9F8B84 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 464;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 94 GYWLSSW 100  
  
RESULT 11  
Q6HNI4 PRELIMINARY; PRT; 465 AA.  
ID Q6HNI4;  
AC Q6HNI4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Probable arginine/ornithine antiporter protein.  
GN Name=arcD; ORFNames=BT9727\_0540;  
OS Bacillus thuringiensis serovar konkukian str. 97-27.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus thuringiensis serovar konkukian.  
OX NCBI\_TaxID=281309;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97-27;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE017355; AAT62417.1; --  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 465 AA; 50153 MW; 534F038C0A379E04 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 96 GYWAANW 102

RESULT 12  
Q6I3F7 PRELIMINARY; PRT; 465 AA.  
ID Q6I3F7;  
AC Q6I3F7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Amino acid permease family protein.  
GN OrderedLocusNames=BAS0596;  
OS Bacillus anthracis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1392;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sterne;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE017225; AAT52924.1; --  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |

Db	96 GYWAANW 102	SQ	SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;	Query Match 89.5%; Score 34; DB 2; Length 465; Best Local Similarity 57.1%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT 13		QY	1 GYWXXXW 7	
Q73DL5		Db	96 GYWAANW 102	
ID Q73DL5	PRELIMINARY; PRT; 465 AA.			
AC Q73DL5;				
DT 05-JUL-2004	(TReMBLrel. 27, Created)			
DT 05-JUL-2004	(TReMBLrel. 27, Last sequence update)			
DT 05-JUL-2004	(TReMBLrel. 27, Last annotation update)			
DE	Amino acid permease family protein.			
GN	OrderedLocusNames=BCE0697;			
OS	Bacillus cereus (strain ATCC 10987).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=222523;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=14960714;			
RA	Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,			
RA	Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,			
RA	Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;			
RT	"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic			
RT	adaptations and a large plasmid related to Bacillus anthracis pX01.";			
RL	Nucleic Acids Res. 32:977-988(2004).			
DR	EMBL; AE017266; AAS39630.1; -.			
DR	TIGR; BCE0697; -.			
DR	InterPro; IPR002293; AA/rel_permeasel.			
DR	InterPro; IPR004841; Permease_region.			
DR	Pfam; PF00324; AA_permease; 1.			
KW	Complete proteome; Transmembrane; Transport.			
SQ	SEQUENCE 465 AA; 50193 MW; C18384E10EBC639D CRC64;			
Query Match 89.5%; Score 34; DB 2; Length 465; Best Local Similarity 57.1%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GYWXXXW 7			
Db	96 GYWAANW 102			
RESULT 14				
Q81HZ7				
ID Q81HZ7	PRELIMINARY; PRT; 465 AA.			
AC Q81HZ7;				
DT 01-JUN-2003	(TReMBLrel. 24, Created)			
DT 01-JUN-2003	(TReMBLrel. 24, Last sequence update)			
DT 01-MAR-2004	(TReMBLrel. 26, Last annotation update)			
DE	Arginine/cornithine antiporter.			
GN	ORFNames=BC0629;			
OS	Bacillus cereus (strain ATCC 14579 / DSM 31).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=226900;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;			
RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,			
RA	Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,			
RA	Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,			
RA	Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,			
RA	Overbeek R., Kyrpides N.C.;			
RT	"Genome sequence of Bacillus cereus and comparative analysis with			
RT	Bacillus anthracis.";			
RL	Nature 423:87-91(2003).			
DR	EMBL; AE017000; AAP07646.1; -.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.			
DR	GO; GO:0006865; P:amino acid transport; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR002293; AA/rel_permeasel.			
DR	InterPro; IPR004841; Permease_region.			
DR	Pfam; PF00324; AA_permease; 1.			
KW	Transmembrane; Transport.			





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OM protein - protein search, using sw model  
Run on: December 29, 2004, 22:08:20 ; Search time 148 Seconds  
(without alignments)  
19.391 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYXXXXWX 8  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2002273 seqs, 358729299 residues  
Total number of hits satisfying chosen parameters: 153769

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	82.1	7	5	ABP53964
2	32	82.1	8	5	ABP53965
3	31	79.5	7	3	AAW76794
4	31	79.5	7	5	ABP53418
5	28	71.8	8	4	ABP24270
6	28	71.8	8	4	ABP15891
7	28	71.8	8	4	ABP15892
8	28	71.8	8	4	ABP24235
9	27	69.2	8	2	AAR32766
10	27	69.2	8	6	ABU61730
11	26	66.7	6	2	AAR93713
12	26	66.7	8	2	AAW27066
13	26	66.7	8	2	AAW02418
14	25	64.1	7	3	AAW76792
15	25	64.1	7	5	ABP53416
16	25	64.1	8	1	AAP61465
17	25	64.1	8	1	AAP90981
18	25	64.1	8	2	AAR14237
19	25	64.1	8	2	AAR15362
20	25	64.1	8	2	AAR10505
21	25	64.1	8	2	AAR26369
22	25	64.1	8	2	AAR27185
23	25	64.1	8	2	AAR27187
24	25	64.1	8	2	AAR27197
25	25	64.1	8	2	AAR23952

26	25	64.1	8	2	AAR40822	Aar40822	Octapepti
27	25	64.1	8	2	AAR41502	Aar41502	Somatosta
28	25	64.1	8	2	AAR31513	Aar31513	Somatosta
29	25	64.1	8	2	AAR31511	Aar31511	Somatosta
30	25	64.1	8	2	AAR42653	Aar42653	Somatosta
31	25	64.1	8	2	AAR56781	Aar56781	Somatosta
32	25	64.1	8	2	AAR76207	Aar76207	Somatosta
33	25	64.1	8	2	AAR76205	Aar76205	Somatosta
34	25	64.1	8	2	AAR85570	Aar85570	Somatosta
35	25	64.1	8	2	AAW18454	Aaw18454	Somatosta
36	25	64.1	8	2	AAW51865	Aaw51865	Somatosta
37	25	64.1	8	2	AAW22044	Aay22044	Somatosta
38	25	64.1	8	2	AAW18229	Aay18229	Somatosta
39	25	64.1	8	2	AAW45740	Aaw45740	Somatosta
40	25	64.1	8	2	AAW97185	Aaw97185	Somatosta
41	25	64.1	8	2	ADH35407	Adh35407	Human som
42	25	64.1	8	2	ADH68008	Adh68008	Somatosta
43	25	64.1	8	2	ADK11160	Adk11160	Somatosta
44	25	64.1	8	2	ADK11282	Adk11282	Somatosta
45	25	64.1	8	2	ADK11283	Adk11283	Somatosta

ALIGNMENTS

RESULT 1  
ABP53964  
ID ABP53964 standard; peptide; 7 AA.  
XX

AC ABP53964;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:67.  
XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnery; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT Misc-difference 4. .6  
FT /note= "X is any amino acid"

XX WO200257299-A2.

XX 25-JUL-2002.

XX 16-JAN-2002; 2002WO-IB0000099.

XX 17-JAN-2001; 2001US-0262476P.

XX (LUDW-) LUDWIG INST CANCER RES.  
XX (LICN ) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;

XX WPI; 2002-691521/74.

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX

PS Claim 21; Page 81; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,

CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 7 AA;  
  
Query Match 82.1%; Score 32; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
Db 1 GYWXXXW 7  
  
RESULT 2  
ABP53965  
ID ABP53965 standard; peptide; 8 AA.  
XX  
AC ABP53965;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:68.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnerary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 4..6 /note= "X is any amino acid"  
FT Misc-difference 8 /note= "any amino acid"  
FT  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
XX Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 22; Page 81; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,

CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 8 AA;  
  
Query Match 82.1%; Score 32; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
Db 1 GYWXXXW 7  
  
RESULT 3  
AAY76794  
ID AAY76794 standard; peptide; 7 AA.  
XX  
AC AAY76794;  
XX  
DT 20-APR-2000 (first entry)  
XX  
DE Somatostatin analogue peptide 3181.  
XX  
KW Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 3 /note= "D-form residue"  
FT Modified-site 7 /note= "Trp-NH2"  
FT  
XX  
PN WO9965508-A1.  
XX  
PD 23-DEC-1999.  
XX  
PF 15-JUN-1999; 99WO-IL000329.  
XX  
PR 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
XX  
PA (PEPT-) PEPTOR LTD.  
XX  
PI Hornik V, Afargan MM, Gellerman G;  
XX  
DR WPI; 2000-136888/12.  
XX  
PT Cyclized somatostatin analogs for inhibiting growth hormone secretion  
PT from anterior pituitary and as antiproliferative agents for the treatment  
PT of tumors.  
XX  
PS Example 11; Page 61; 82pp; English.  
XX  
CC This sequence represents a somatostatin analogue of the invention. The  
CC invention relates to a backbone cyclised somatostatin analogue that has  
CC one building unit containing a nitrogen atom of the peptide backbone  
CC connected to a bridging group comprising an amide, thioether, thioester

CC or disulphide. At least one building unit is connected via a bridging  
CC group to form a cyclic structure with a moiety selected from a second  
CC building unit, side chain of or N-terminal amino acid residue. A  
CC composition containing the analogue may be used for preventing disorders  
CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
CC associated complications, gastrointestinal disorders, inflammatory  
CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
CC analogue is used for imaging the existence of metastases. Somatostatin  
CC analogues can be used for the treatment of patients with hormone-secreting  
CC and hormone-dependent tumours. They reduce diarrhoea through the  
CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
CC effect on intestinal secretion. Somatostatin analogues selective to type  
CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
CC and restenosis. The analogues are metabolically stable, selective in  
CC their in-vivo activities and safe  
XX  
SQ Sequence 7 AA;

Query Match 79.5%; Score 31; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
||| |  
Db 1 GYWKVCW 7

RESULT 4  
ABP53418  
ID ABP53418 standard; peptide; 7 AA.

XX ABP53418;

XX 19-NOV-2002 (first entry)

XX Backbone cyclised somatostatin analogue PTR 3181.

XX Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
KW somatotropin release inhibiting factor; somatostatin receptor subtype;  
KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;  
KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
KW pancreatitis; post-surgical pain.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminally modified with Fmoc  
(fluorenylmethoxycarbonyl)"

FT Misc-difference 3 /note= "D form residue"

FT Modified-site 7 /note= "amidated"

XX US2002052315-A1.

XX 02-MAY-2002.

XX 13-DEC-2000; 2000US-00734583.

XX 19-JUN-1998; 98US-00100360.

XX 02-DEC-1998; 98US-00203389.

XX 15-JUN-1999; 99WO-IL000329.

XX (HORN/) HORN V.

XX (AFAR/) AFARGAN M M.

XX (GELL/) GELLERMAN G.

XX Hornik V, Afargan MM, Gellerman G;

XX WPI; 2002-681319/73.  
DR  
XX New backbone cyclized somatostatin analogs are e.g. useful in the  
XX treatment of atherosclerosis, autoimmune diseases and cancers.  
PT  
XX Example 12; Page 21; 30pp; English.  
PS

CC The present invention describes backbone cyclised somatostatin analogues  
CC (I) that incorporates at least one building unit containing one nitrogen  
CC atom of the peptide backbone connected to a bridging group (comprising an  
CC amide, thioether, thioester or disulfide) where at least one building  
CC unit is connected via the bridging group to form a cyclic structure with  
CC a moiety selected from the group consisting of a second building unit,  
CC the side chain of an amino acid residue of the sequence or the N-terminal  
CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive, and  
CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and  
CC can be used as a somatostatin receptor ligand. (I) are useful in the  
CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-  
CC associated complications, endocrine disorders, inflammation,  
CC gastrointestinal disorders, pancreatitis, post-surgical pain, and  
CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging  
CC the existence of metastases, it being labeled with a detectable probe.  
CC The present sequence represents a backbone cyclised somatostatin analogue  
CC from the present invention  
XX  
SQ Sequence 7 AA;

Query Match 79.5%; Score 31; DB 5; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
||| |  
Db 1 GYWKVCW 7

RESULT 5  
ABP24270

ID ABP24270 standard; peptide; 8 AA.

XX ABP24270;

XX 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A24 motif pol peptide #78.

XX HIV; HIV-1; human immunodeficiency virus; env; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX Claim 32; Page 366; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. (I) may  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 8 AA;  
  
Query Match 71.8%; Score 28; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWXXXW 7  
|||  
Db 2 YWQATW 7  
  
RESULT 6  
ABP15891  
ID ABP15891 standard; peptide; 8 AA.  
XX  
AC ABP15891;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 super motif pol peptide #71.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 194; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 8 AA;  
  
Query Match 71.8%; Score 28; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWXXXW 7  
|||  
Db 2 YWQATW 7  
  
RESULT 7  
ABP15892  
ID ABP15892 standard; peptide; 8 AA.  
XX  
AC ABP15892;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 super motif pol peptide #72.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 194; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to



CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variations. The groups for inclusion in  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 8 AA;  
  
Query Match 71.8%; Score 28; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWXXXW 7  
Db |||  
2 YWQATW 7  
  
RESULT 8  
ABP24235  
ID ABP24235 standard; peptide; 8 AA.  
XX  
AC ABP24235;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 motif pol peptide #43.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 366; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variations. The groups for inclusion in  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 8 AA;  
  
Query Match 71.8%; Score 28; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWXXXW 7  
Db |||  
2 YWQATW 7  
  
RESULT 9  
AAR32766  
ID AAR32766 standard; peptide; 8 AA.  
XX  
AC AAR32766;  
XX  
DT 25-MAR-2003 (revised)  
DT 30-JUN-1993 (first entry)  
XX  
DE Lanthionine-peptide.  
XX  
KW Thioether; bond; bridge; monosulfide; monosulphide; disulfide;  
KW disulphide.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "D-form residue"  
FT Modified-site 2..7 /note= "thioether bond between A2 and A7 to form  
FT lanthionine"  
FT Misc-difference 4 /note= "D-form residue"  
FT Modified-site 8 /note= "amidated C-terminal"  
XX  
PN WO9303056-A1.  
XX  
PD 18-FEB-1993.  
XX  
PF 06-AUG-1992; 92WO-EP001789.  
XX  
PR 09-AUG-1991; 91US-00742908.  
XX  
PA (KOLB/) KOLBECK W.  
XX  
PI Goodman M, Osapay G;  
XX  
DR WPI; 1993-076437/09.  
XX  
PT New lanthionine bridged peptide derivs. - are analogues of ACTH,  
PT angiotensin, neuro:peptide(s), bombesin, bradykinin, etc.  
XX



PS Claim 7; Page 27; 33pp; English.

XX The lanthionine bridged peptide is an analog cpd. of a naturally

CC occurring biologically active peptide, having improved properties.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 8 AA;

Query Match 69.2%; Score 27; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7

Db 3 YWKVAW 8

RESULT 10

ABU61730

ID ABU61730 standard; peptide; 8 AA.

XX

AC ABU61730;

XX

DT 13-AUG-2003 (first entry)

XX

DE Lanthionine bridged peptide #25.

XX

KW Lanthionine bridged peptide; monosulphide bridge; thioether bond;

KW improved biological activity; vasopressin; somatostatin; enkephalin;

KW endothelin; pharmaceutically active compound.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "D-form residue. Modified by H"

FT Modified-site 2. .7

FT /note= "Residues 2 and 7 linked by a lanthionine bridge"

FT Misc-difference 4

FT /note= "D-form residue"

FT Modified-site 8

FT /note= "Modified by C-terminal amide (NH2) group"

XX

PN US2002165132-A1.

XX

PD 07-NOV-2002.

XX

PF 10-MAY-2001; 2001US-00852870.

XX

PR 09-AUG-1991; 91US-00742908.

PR 28-JAN-1993; 93US-00021606.

PR 06-JUN-1995; 95US-00467472.

PR 26-AUG-1999; 99US-00384061.

XX

PA (GOOD/) GOODMAN M.

PA (OSAP/) OSAPAY G.

XX

PI Goodman M, Osapay G;

XX

DR WPI; 2003-391607/37.

XX

PT Novel lanthionine-bridged biologically active peptides e.g. vasopressin,

PT somatostatin or enkephalin, useful as pharmaceutically active compounds.

XX

PS Claim 16; Page 19; 24pp; English.

XX

CC The present invention relates to lanthionine bridged peptides which are

CC analogues of peptide compounds comprising a disulphide bridge. The

CC disulphide bridge is replaced by monosulphide bridge or thioether bond,

CC designated a lanthionine bridge. Such analogues or lanthionine bridged

CC peptides have improved biological activity compared to the original

CC peptide compounds e.g. vasopressin, somatostatin, enkephalin, and

CC endothelin. The lanthionine-bridged peptides are useful as

CC pharmaceutically active compounds. The present sequence represents a

CC lanthionine bridged peptide

XX

SQ Sequence 8 AA;

Query Match 69.2%; Score 27; DB 6; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7

Db 3 YWKVAW 8

RESULT 11

AAR93713

ID AAR93713 standard; peptide; 6 AA.

XX

AC AAR93713;

XX

DT 10-MAY-1996 (first entry)

XX

DE Cyclo[-Tyr-trp-Leu-Arg-Gly-Trp-].

XX

KW neurokinin A antagonist; tachykinin; respiratory disease; asthma;

KW analgesic; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "not an N-terminal amino acid, but condensed with

FT Trp(6) to form a cyclic peptide"

FT Misc-difference 2

FT /note= "D-form residue"

FT Modified-site 6

FT /note= "not a C-terminal amino acid, but condensed with

FT Tyr(1) to form a cyclic peptide"

XX

PN WO9521187-A1.

XX

PD 10-AUG-1995.

XX

PF 10-JAN-1995; 95WO-US000296.

XX

PR 03-FEB-1994; 94US-00191571.

XX

PA (RICH ) MERRELL DOW PHARM INC.

XX

PI Owen TJ, Kudlacz EM, Buck SH, Harbeson SL;

XX

DR WPI; 1995-336695/43.

XX

PT New cyclic peptide derivs. - are neurokinin A and tachykinin antagonists

PT useful e.g. for treating asthma or as analgesics.

XX

PS Claim 8; Page 69; 82pp; English.

XX

CC The patent describes novel cyclic hexapeptide and octapeptide compounds

CC which are antagonists of neurokinin A and which are useful medically as

CC analgesics and for treating respiratory diseases such as asthma. The

CC present sequence represents a specifically preferred example of the new

CC peptides

XX

SQ Sequence 6 AA;

Query Match 66.7%; Score 26; DB 2; Length 6;

Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7

Db 1 YWLRGW 6

RESULT 12  
AAW27066  
ID AAW27066 standard; peptide; 8 AA.  
XX  
AC AAW27066;  
XX  
DT 17-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 28-FEB-1998 (first entry)  
XX  
DE Galactanase peptide motif.  
XX  
KW Galactanase; fruit juice; vegetable juice; wine; pectin; depectinisation;  
KW animal feed; foodstuff.  
XX  
OS Corynascus heterothallicus; strain CBS 117.65.  
OS Humicola insolens; strain DSM 1800.  
XX  
PN WO9732014-A1.  
XX  
PD 04-SEP-1997.  
XX  
XX 28-FEB-1997; 97WO-DK000092.  
XX  
PR 01-MAR-1996; 96DK-00000233.  
PR 01-MAR-1996; 96DK-00000235.  
XX  
PA (NOVO ) NOVO-NORDISK AS.  
XX  
XX Kofod LV, Kauppinen MS, Andersen LN, Clausen IG, Muellertz A;  
PI WPI; 1997-448686/41.  
XX  
DR Fungal galactanase and related DNA - useful in animal feed industry and  
XX fruit juice depectinisation.  
XX  
PS Claim 7; Page 58; 67pp; English.  
XX  
CC This peptide comprises a motif located at amino acid residues 312-319 of  
CC the galactanase of Myceliophthora thermophila CBS 117.65 (see AAW27063)  
CC and at amino acid residues 311-318 of the galactanase of Humicola  
CC insolens DSM 1800 (see AAW27064). Another motif (see AAW27065) has also  
CC been identified. These motifs are characteristic of galactanases of fungi  
CC of the order Sordariales. PCR primers (see AAT85060-61) based on the  
CC motifs can be used to identify galactanase enzymes in Sordariales fungi.  
CC Such enzymes have an optimum pH above 5.8 and are useful in the food and  
CC feed industries, as well as in wine and juice processing. (Updated on 25-  
CC MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS  
CC field)  
XX  
SQ Sequence 8 AA;  
Query Match 66.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 YWXXXW 7  
Db 2 YWEPW 7  
RESULT 13  
AAW02418  
ID AAW02418 standard; peptide; 8 AA.  
XX  
AC AAW02418;  
XX  
DT 12-JUL-1999 (first entry)  
XX  
DE Somatostatin analogue peptide.  
XX  
KW Metallo-construct; metal ion-binding backbone; cyclic;  
KW biological function domain; conformational restriction; radiotherapeutic;  
XX combinatorial chemistry.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "D-form residue"  
FT Modified-site 3.8  
FT Misc-difference 4 /note= "linked with GGGC, GGC, GGGh or GGH"  
FT Misc-difference 7 /note= "D-form residue"  
FT Modified-site 7 /label= Orn  
FT /note= "Ornithine"  
XX  
PN WO9640293-A1.  
XX  
XX 19-DEC-1996.  
PD  
XX  
PF 06-JUN-1996; 96WO-US009840.  
XX  
PR 07-JUN-1995; 95US-00476652.  
PR 05-JUN-1996; 96US-00660697.  
XX  
PA (RHOM-) RHOMED INC.  
XX  
PI Sharma SD;  
XX  
DR WPI; 1997-077237/07.  
XX  
XX Metallo-constructs comprising a metal ion-binding backbone for complexing  
PT metals - and a biological function domain which may be converted from  
PT inactive to active form on binding of the construct to a metal ion.  
XX  
PS Disclosure; Page 21; 142pp; English.  
XX  
CC The specification describes a metallo-construct, which may be a peptide,  
CC comprising metal ion-binding backbone for complexing with a metal ion and  
CC a biological function domain which is conformationally constrained upon  
CC complexing the metal ion-binding backbone with a metal ion. The  
CC peptide/metal ion complexes are less susceptible to proteolysis than the  
CC uncomplexed peptide. The peptides lack conformational restriction if not  
CC complexed to a metal ion, so that the uncomplexed peptides are either  
CC inactive or low in potency. The complexed peptides may also exhibit  
CC altered biodistribution profiles, rate of clearance from the body and  
CC bioavailability. The constructs/peptides are useful as biological,  
CC therapeutic, diagnostic imaging and radiotherapeutic agents, or in  
CC combinatorial chemistry methods. The present cyclic peptide exemplifies  
CC the peptides of the invention  
XX  
SQ Sequence 8 AA;  
Query Match 66.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 YWXXXW 7  
Db 3 YWKVXW 8  
RESULT 14  
AAW76792  
ID AAW76792 standard; peptide; 7 AA.  
XX  
AC AAW76792;  
XX  
DT 20-APR-2000 (first entry)  
XX  
DE Somatostatin analogue peptide 3177.  
XX

KW Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.  
XX  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 3 /note= "D-form residue"  
FT Modified-site 7 /note= "Trp-NH2"  
FT  
FT  
XX WO9965508-A1.  
PN  
XX  
PD 23-DEC-1999.  
XX  
PF 15-JUN-1999; 99WO-IL000329.  
XX  
PR 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
XX  
PA (PEPT-) PEPTOR LTD.  
XX  
XX  
PI Hornik V, Afargan MM, Gellerman G;  
XX  
DR WPI; 2000-136888/12.  
XX  
XX  
PT Cyclized somatostatin analogs for inhibiting growth hormone secretion  
PT from anterior pituitary and as antiproliferative agents for the treatment  
PT of tumors.  
XX  
PS Example 11; Page 61; 82pp; English.  
XX  
CC This sequence represents a somatostatin analogue of the invention. The  
CC invention relates to a backbone cyclised somatostatin analogue that has  
CC one building unit containing a nitrogen atom of the peptide backbone  
CC connected to a bridging group comprising an amide, thioether, thioester  
CC or disulphide. At least one building unit is connected via a bridging  
CC group to form a cyclic structure with a moiety selected from a second  
CC building unit, side chain of or N-terminal amino acid residue. A  
CC composition containing the analogue may be used for preventing disorders  
CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
CC associated complications, gastrointestinal disorders, inflammatory  
CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
CC analogue is used for imaging the existence of metastases. Somatostatin  
CC analogues can be used for the treatment patients with hormone-secreting  
CC and hormone-dependent tumours. They reduce diarrhoea through the  
CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
CC effect on intestinal secretion. Somatostatin analogues selective to type  
CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
CC and restenosis. The analogues are metabolically stable, selective in  
CC their in-vivo activities and safe  
XX  
SQ Sequence 7 AA;  
  
Query Match 64.1%; Score 25; DB 3; Length 7;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWXXXW 7  
|||  
Db 2 YWKVCW 7  
  
RESULT 15  
ABP53416  
ID ABP53416 standard; peptide; 7 AA.  
XX

AC ABP53416;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Backbone cyclised somatostatin analogue PTR 3177.  
XX  
KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
KW somatotropin release inhibiting factor; somatostatin receptor subtype;  
KW synthesis; antiarteriosclerotic; immunosuppressive; cyostatic; cancer;  
KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
KW pancreatitis; post-surgical pain.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 3 /note= "D form residue"  
FT Modified-site 7 /note= "amidated"  
FT  
XX  
PN US2002052315-A1.  
XX  
PD 02-MAY-2002.  
XX  
PF 13-DEC-2000; 2000US-00734583.  
XX  
PR 19-JUN-1998; 98US-00100360.  
PR 02-DEC-1998; 98US-00203389.  
PR 15-JUN-1999; 99WO-IL000329.  
XX  
PA (HORN/) HORNIK V.  
PA (AFAR/) AFARGAN M M.  
PA (GELL/) GELLERMAN G.  
XX  
PI Hornik V, Afargan MM, Gellerman G;  
XX  
DR WPI; 2002-681319/73.  
XX  
PT New backbone cyclized somatostatin analogs are e.g. useful in the  
PT treatment of atherosclerosis, autoimmune diseases and cancers.  
XX  
PS Example 12; Page 21; 30pp; English.  
XX  
CC The present invention describes backbone cyclised somatostatin analogues  
CC (I) that incorporates at least one building unit containing one nitrogen  
CC atom of the peptide backbone connected to a bridging group (comprising an  
CC amide, thioether, thioester or disulfide) where at least one building  
CC unit is connected via the bridging group to form a cyclic structure with  
CC a moiety selected from the group consisting of a second building unit,  
CC the side chain of an amino acid residue of the sequence or the N-terminal  
CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,  
CC cyostatic, antidiabetic, antiinflammatory and analgesic activities, and  
CC can be used as a somatostatin receptor ligand. (I) are useful in the  
CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-  
CC associated complications, endocrine disorders, inflammation,  
CC gastrointestinal disorders, pancreatitis, post-surgical pain, and  
CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging  
CC the existence of metastases, it being labeled with a detectable probe.  
CC The present sequence represents a backbone cyclised somatostatin analogue  
CC from the present invention  
XX  
SQ Sequence 7 AA;  
  
Query Match 64.1%; Score 25; DB 5; Length 7;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWXXXW 7  
|||  
Db 2 YWKVCW 7

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(without alignments)  
14.339 Million cell updates/sec

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Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	61.5	5	1 US-08-353-400-27	Sequence 27, Appl
2	24	61.5	5	4 US-08-753-750B-38	Sequence 38, Appl
3	24	61.5	5	6 5185431-15	Patent No. 5185431
4	24	61.5	6	1 US-07-718-577-6	Sequence 6, Appli
5	24	61.5	7	1 US-07-973-235A-30	Sequence 30, Appl
6	24	61.5	7	1 US-08-443-640-16	Sequence 16, Appl
7	24	61.5	7	2 US-08-462-720-30	Sequence 30, Appl
8	24	61.5	7	4 US-09-388-788-2	Sequence 2, Appli
9	24	61.5	7	4 US-09-069-827A-94	Sequence 94, Appl
10	24	61.5	7	4 US-09-563-222C-53	Sequence 53, Appl
11	24	61.5	8	3 US-08-467-472C-5	Sequence 5, Appli
12	24	61.5	8	3 US-08-467-472C-6	Sequence 6, Appli
13	24	61.5	8	3 US-08-586-670A-17	Sequence 17, Appl
14	24	61.5	8	3 US-09-384-061-5	Sequence 5, Appli
15	24	61.5	8	3 US-09-384-061-6	Sequence 6, Appli
16	24	61.5	8	4 US-09-125-641-1	Sequence 1, Appli
17	24	61.5	8	4 US-09-125-641-2	Sequence 2, Appli
18	24	61.5	8	4 US-09-852-870A-5	Sequence 5, Appli
19	23	59.0	8	3 US-08-467-472C-7	Sequence 7, Appli
20	23	59.0	8	3 US-08-467-472C-8	Sequence 8, Appli
21	23	59.0	8	3 US-09-384-061-7	Sequence 7, Appli
22	23	59.0	8	3 US-09-384-061-8	Sequence 8, Appli
23	23	59.0	8	4 US-09-852-870A-7	Sequence 7, Appli
24	22	56.4	6	2 US-08-446-345-12	Sequence 12, Appl
25	22	56.4	6	3 US-08-951-260A-2	Sequence 2, Appli
26	22	56.4	6	3 US-08-884-569A-11	Sequence 11, Appl
27	22	56.4	6	3 US-08-884-569A-14	Sequence 14, Appl

28	22	56.4	6	4 US-09-430-626A-2	Sequence 2, Appli
29	22	56.4	6	4 US-09-361-096A-46	Sequence 46, Appl
30	22	56.4	6	4 US-09-743-492A-5	Sequence 5, Appli
31	22	56.4	6	4 US-10-243-687-2	Sequence 2, Appli
32	22	56.4	7	2 US-08-652-971-5	Sequence 5, Appli
33	22	56.4	7	2 US-08-991-258A-5	Sequence 5, Appli
34	22	56.4	7	2 US-08-769-399-5	Sequence 5, Appli
35	22	56.4	7	3 US-08-991-953A-5	Sequence 5, Appli
36	22	56.4	8	3 US-09-100-804-5	Sequence 5, Appli
37	22	56.4	8	3 US-09-081-345-5	Sequence 5, Appli
38	22	56.4	8	3 US-09-095-443-6	Sequence 6, Appli
39	22	56.4	8	4 US-09-794-529B-1	Sequence 1, Appli
40	22	56.4	8	4 US-09-794-517A-1	Sequence 1, Appli
41	22	56.4	8	4 US-09-011-645E-1	Sequence 1, Appli
42	22	56.4	8	4 US-09-794-832-1	Sequence 1, Appli
43	22	56.4	8	4 US-09-680-806A-1	Sequence 1, Appli
44	22	56.4	8	4 US-09-552-868-1	Sequence 1, Appli
45	22	56.4	8	4 US-09-636-295-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-353-400-27  
; Sequence 27, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,400  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9324819.3  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9411089.7  
; FILING DATE: 03-JUN-1994  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-353-400-27  
  
Query Match 61.5%; Score 24; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GYW 3  
|||  
Db 1 GYW 3  
  
RESULT 2  
US-08-753-750B-38  
; Sequence 38, Application US/08753750B  
; Patent No. 6610506  
; GENERAL INFORMATION:  
; APPLICANT: Io, Reggie Y.C.  
; APPLICANT: Schryvers, Anthony B.  
; APPLICANT: Potter, Andrew A.  
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF

```
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pasteurella haemolytica
US-08-753-750B-38

Query Match          61.5%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYW 3
      |||
Db      3 GYW 5

RESULT 3
5185431-15
;Patent No. 5185431
; APPLICANT: YOSHIMATSU, KENTARO;SHIKATA, YASUSHI;TANAKA, ISAO;
;HASEGAWA, YOSHIKAZU;SETO, TOSHIO;OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,841
; FILING DATE: 11-AUG-1989
;SEQ ID NO:15:
; LENGTH: 5
5185431-15

Query Match          61.5%; Score 24; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYW 3
      |||
Db      2 GYW 4

RESULT 4
US-07-718-577-6
; Sequence 6, Application US/07718577
; Patent No. 5432018
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Barrett, Ronald W.
; TITLE OF INVENTION: PEPTIDE LIBRARY AND
; TITLE OF INVENTION: SCREENING SYSTEMS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street
; STREET: Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/07/718,577
; FILING DATE: 19910620
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/541,108
; FILING DATE: 20-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-25-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-718-577-6

Query Match          61.5%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYW 3
      |||
Db      2 GYW 4

RESULT 5
US-07-973-235A-30
; Sequence 30, Application US/07973235A
; Patent No. 5491130
; GENERAL INFORMATION:
; APPLICANT: David D. Roberts, et al.
; TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and
; TITLE OF INVENTION: Related Collagen-Binding Proteins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,235A
; FILING DATE: 19921110
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert L. Price
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)684-1111
; TELEFAX: (703)684-1124
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACIDS
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-973-235A-30

Query Match          61.5%; Score 24; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
```

Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXW 7  
| | | |  
Db 1 GGWSKSW 7

## RESULT 6

US-08-443-640-16  
; Sequence 16, Application US/08443640  
; Patent No. 5691140  
; GENERAL INFORMATION:  
; APPLICANT: NOREN, CHRISTOPHER J.  
; APPLICANT: EVANS, PAUL D.  
; TITLE OF INVENTION: BIDIRECTIONAL IN VITRO TRANSCRIPTION  
; TITLE OF INVENTION: VECTORS UTILIZING A SINGLE RNA POLYMERASE FOR BOTH  
; TITLE OF INVENTION: DIRECTIONS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEW ENGLAND BIOLABS, INC  
; STREET: 32 TOZER ROAD  
; CITY: BEVERLY  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,640  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILLIAMS, GREGORY D.  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: NEB-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 927-5054  
; TELEFAX: (508) 927-1705  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-443-640-16

Query Match 61.5%; Score 24; DB 1; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GYXXXXW 7  
| | | |  
Db 1 GEWRFAW 7

## RESULT 7

US-08-462-720-30  
; Sequence 30, Application US/08462720  
; Patent No. 5849701  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, David D.  
; APPLICANT: Kruttsch, Henry C.  
; APPLICANT: Sipes, John M.  
; APPLICANT: Guo, Neng-hua  
; APPLICANT: Negre, Eric  
; TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and  
; TITLE OF INVENTION: Related Collagen-Binding Proteins  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,720  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 015280-023110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-462-720-30

Query Match 61.5%; Score 24; DB 2; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXW 7  
| | | |  
Db 1 GGWSKSW 7

## RESULT 8

US-09-388-788-2  
; Sequence 2, Application US/09388788  
; Patent No. 6429359  
; GENERAL INFORMATION:  
; APPLICANT: LAMPPA, GAYLE  
; TITLE OF INVENTION: PRODUCTION OF CELLULASE IN PLASTIDS OF TRANSGENIC  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 21459/90301  
; CURRENT APPLICATION NUMBER: US/09/388,788  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein  
; OTHER INFORMATION: Construct  
US-09-388-788-2

Query Match 61.5%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
| | |  
Db 5 GYW 7

## RESULT 9

US-09-069-827A-94

; Sequence 94, Application US/09069827A  
; Patent No. 6617114  
; GENERAL INFORMATION:  
; APPLICANT: FOWLKES, Dana M  
; KAY, Brian K  
; FRELINGER, Jeffrey A  
; HYDE-DERUYSCHE, Robin P  
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING  
; COMPLEMENTARY COMBINATORIAL LIBRARIES  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 624 Ninth Street N.W., Suite 300  
; City: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069,827A  
; FILING DATE: 30-Apr-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/050,359  
; FILING DATE: 31-MAR-1998  
; APPLICATION NUMBER: PCT/US97/19638  
; FILING DATE: 31-OCT-1997  
; APPLICATION NUMBER: US 08/740,671  
; FILING DATE: 31-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOWLKES=4C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:  
US-09-069-827A-94  
  
Query Match 61.5%; Score 24; DB 4; Length 7;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 YWXXW 7  
Db 1 YWPDW 6  
  
RESULT 10  
US-09-563-222C-53  
; Sequence 53, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/09/563,222C  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222C-53  
  
Query Match 61.5%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GYW 3  
Db 2 GYW 4  
  
RESULT 11  
US-08-467-472C-5  
; Sequence 5, Application US/08467472C  
; Patent No. 6028168  
; GENERAL INFORMATION:  
; APPLICANT: GOODMAN, MURRAY  
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY  
; STREET: 99 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" FLOPPY DISC  
; COMPUTER: COMPAQ - IBM COMPATIBLE  
; OPERATING SYSTEM: MS-DOS Version 6.2  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,472C  
; FILING DATE: 6-JUNE-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/742,908  
; FILING DATE: 9-AUGUST-1991  
; APPLICATION NUMBER: US 08/021,606  
; FILING DATE: 28-JANUARY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINSON, WILLIAM R.  
; REGISTRATION NUMBER: 27,224  
; REFERENCE/DOCKET NUMBER: LKR-9122B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 697-3355  
; TELEFAX: (212) 557-5635  
; TELEX: NONE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE:  
; DESCRIPTION: PEPTIDE  
; HYPOTHETICAL: N/A  
; ANTI-SENSE: N/A  
; FRAGMENT TYPE: INTERNAL  
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -  
; ORIGINAL SOURCE: INC.,  
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE  
; POSITION IN GENOME: N/A  
; FEATURE:  
; NAME/KEY: ENANTIOMER  
; LOCATION: -4



IDENTIFICATION METHOD: amino acid analysis  
IDENTIFICATION METHOD: and  
IDENTIFICATION METHOD: mass spectrometry  
OTHER INFORMATION: water is removed and  
OTHER INFORMATION: thereby  
OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
PUBLICATION INFORMATION:  
AUTHORS: JUNG, GUNTHER  
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
JOURNAL: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 865 - 869  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: SHIBA, TETSUO  
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES  
JOURNAL: BIOPOLYMERS  
VOLUME: JOHN WILEY AND SONS, INC.  
ISSUE: SUPPLEMENTARY  
PAGES: 511 - 519  
DATE: 1986  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: BEAN, MARK F.  
TITLE: IDENTIFICATION OF A THIOETHER  
TITLE: BY-PRODUCT  
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE  
TITLE: BY  
TITLE: TANDEM MASS SPECTROMETRY  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
JOURNAL: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 443 - 445  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE  
US-08-467-472C-5  
Query Match 61.5%; Score 24; DB 3; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3.8e+05;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 YWXXW 7  
Db 3 FWKTSW 8  
RESULT 12  
US-08-467-472C-6  
Sequence 6, Application US/08467472C  
Patent No. 6028168  
GENERAL INFORMATION:  
APPLICANT: GOODMAN, MURRAY  
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY  
STREET: 99 PARK AVENUE

CITY: NEW YORK  
STATE: NY  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" FLOPPY DISC  
COMPUTER: COMPAQ - IBM COMPATIBLE  
OPERATING SYSTEM: MS-DOS Version 6.2  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,472C  
FILING DATE: 6-JUNE-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/742,908  
FILING DATE: 9-AUGUST-1991  
APPLICATION NUMBER: US 08/021,606  
FILING DATE: 28-JANUARY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINSON, WILLIAM R.  
REGISTRATION NUMBER: 27,224  
REFERENCE/DOCKET NUMBER: LKR-9122B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 697-3355  
TELEFAX: (212) 557-5635  
TELEX: NONE  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE:  
DESCRIPTION: PEPTIDE  
HYPOTHETICAL: N/A  
ANTI-SENSE: N/A  
FRAGMENT TYPE: INTERNAL  
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -  
ORIGINAL SOURCE: INC.,  
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104  
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE  
POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY: ENANTIOMER  
LOCATION: -4  
IDENTIFICATION METHOD: amino acid analysis  
IDENTIFICATION METHOD: and  
IDENTIFICATION METHOD: mass spectrometry  
OTHER INFORMATION: water is removed and  
OTHER INFORMATION: thereby  
OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
PUBLICATION INFORMATION:  
AUTHORS: JUNG, GUNTHER  
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
JOURNAL: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 865 - 869  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: SHIBA, TETSUO  
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES  
JOURNAL: BIOPOLYMERS  
VOLUME: JOHN WILEY AND SONS, INC.  
ISSUE: SUPPLEMENTARY  
PAGES: 511 - 519  
DATE: 1986  
DOCUMENT NUMBER:



; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-6

Query Match 61.5%; Score 24; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 3.8e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXW 7
Db 3 FWKTSW 8

RESULT 13
US-08-586-670A-17
; Sequence 17, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: Modified-site
; LOCATION: 1..2
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Phe is in the D conformation and is
; OTHER INFORMATION: linked to DTPA;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
; OTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the
; OTHER INFORMATION: D conformation;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7..8
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The carboxyl group of the C-terminal
; OTHER INFORMATION: Thr is reduced to an alcohol;
US-08-586-670A-17

Query Match 61.5%; Score 24; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3
Db 2 GYW 4

RESULT 14
US-09-384-061-5
; Sequence 5, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE

; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; TITLE: TANDEM MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
; US-09-384-061-5

Query Match 61.5%; Score 24; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 3.8e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXXW 7
:|
Db 3 FWKTSW 8

RESULT 15

US-09-384-061-6
; Sequence 6, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:

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; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
;
US-09-384-061-6
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Query Match          61.5%; Score 24; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 3.8e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY      2 YWXXXW 7
      :|_|
Db      3 FWKTSW 8
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Search completed: December 29, 2004, 22:27:50  
Job time : 38 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 22:27:17 ; Search time 140 Seconds  
(without alignments)  
20.556 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYXXXXWX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 83711

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	82.1	7	13 US-10-046-922-67	Sequence 67, Appl
2	32	82.1	8	13 US-10-046-922-68	Sequence 68, Appl
3	25	64.1	8	14 US-10-190-082-586	Sequence 586, App
4	24	61.5	5	15 US-10-436-549-496	Sequence 496, App
5	24	61.5	5	15 US-10-436-549-525	Sequence 525, App
6	24	61.5	5	16 US-10-712-425-496	Sequence 496, App
7	24	61.5	5	16 US-10-712-425-525	Sequence 525, App
8	24	61.5	6	15 US-10-418-943-48	Sequence 48, Appl
9	24	61.5	6	16 US-10-346-737A-45	Sequence 45, Appl
10	24	61.5	7	9 US-09-884-767A-38	Sequence 38, Appl
11	24	61.5	7	10 US-09-563-222-53	Sequence 53, Appl
12	24	61.5	7	15 US-10-403-938-27	Sequence 27, Appl
13	24	61.5	7	16 US-10-475-853-6	Sequence 6, Appli

14	24	61.5	7	17	US-10-783-950-53	Sequence 53, Appl
15	24	61.5	8	9	US-09-852-870A-5	Sequence 5, Appli
16	24	61.5	8	14	US-10-050-902-179	Sequence 179, App
17	24	61.5	8	14	US-10-050-902-180	Sequence 180, App
18	24	61.5	8	14	US-10-050-898-179	Sequence 179, App
19	24	61.5	8	14	US-10-050-898-180	Sequence 180, App
20	24	61.5	8	14	US-10-082-014-279	Sequence 279, App
21	24	61.5	8	14	US-10-372-076-133	Sequence 133, App
22	24	61.5	8	15	US-10-367-580-267	Sequence 267, App
23	24	61.5	8	15	US-10-367-593-267	Sequence 267, App
24	24	61.5	8	15	US-10-367-594-267	Sequence 267, App
25	24	61.5	8	15	US-10-367-654-267	Sequence 267, App
26	24	61.5	8	15	US-10-367-658-267	Sequence 267, App
27	24	61.5	8	15	US-10-367-668-267	Sequence 267, App
28	24	61.5	8	15	US-10-617-876-31	Sequence 31, Appl
29	24	61.5	8	15	US-10-617-876-32	Sequence 32, Appl
30	24	61.5	8	16	US-10-367-674-267	Sequence 267, App
31	24	61.5	8	16	US-10-677-074-133	Sequence 133, App
32	23	59.0	7	17	US-10-858-271-10	Sequence 10, Appl
33	23	59.0	8	9	US-09-852-870A-7	Sequence 7, Appli
34	22	56.4	5	15	US-10-243-613-84	Sequence 84, Appl
35	22	56.4	6	13	US-10-087-993-1	Sequence 1, Appli
36	22	56.4	6	14	US-10-243-687-2	Sequence 2, Appli
37	22	56.4	6	14	US-10-314-232-46	Sequence 46, Appl
38	22	56.4	7	14	US-10-190-082-65	Sequence 65, Appl
39	22	56.4	7	14	US-10-190-082-76	Sequence 76, Appl
40	22	56.4	8	9	US-09-822-295-5	Sequence 5, Appli
41	22	56.4	8	10	US-09-794-517-1	Sequence 1, Appli
42	22	56.4	8	10	US-09-794-529-1	Sequence 1, Appli
43	22	56.4	8	10	US-09-794-832-1	Sequence 1, Appli
44	22	56.4	8	10	US-09-095-478-12	Sequence 12, Appl
45	22	56.4	8	14	US-10-020-215-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-10-046-922-67  
; Sequence 67, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X at position 4-6 is any amino acid  
US-10-046-922-67

Query Match 82.1%; Score 32; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYXXXXW 7  
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Db 1 GYXXXXW 7

RESULT 2  
US-10-046-922-68  
; Sequence 68, Application US/10046922

; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 68  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-68

Query Match 82.1%; Score 32; DB 13; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7  
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Db 1 GYXXXXXW 7

RESULT 3  
US-10-190-082-586  
; Sequence 586, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Held, Heike A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: P1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/303,634  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO 586  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-586

Query Match 64.1%; Score 25; DB 14; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
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Db 3 YWEYWW 8

RESULT 4  
US-10-436-549-496  
; Sequence 496, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.

; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: ENGE-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 496  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-496

Query Match 61.5%; Score 24; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
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Db 1 GYW 3

RESULT 5  
US-10-436-549-525  
; Sequence 525, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.  
; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: ENGE-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01



; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 525  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-525

Query Match 61.5%; Score 24; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
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Db 2 GYW 4

RESULT 6

US-10-712-425-496  
; Sequence 496, Application US/10712425  
; Publication No. US20040180380A1  
; GENERAL INFORMATION:

; APPLICANT: LEE, FRANK D.

; APPLICANT: MENG, XUN

; APPLICANT: LIVINGSTON, DAVID

; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN

; TITLE OF INVENTION: MODIFICATION ANALYSIS

; FILE REFERENCE: ENGE-P02-001

; CURRENT APPLICATION NUMBER: US/10/712,425

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/379,626

; PRIOR FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: 60/393,137

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,197

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,211

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,223

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,233

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,235

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,280

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/430,948

; PRIOR FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 60/433,319

; PRIOR FILING DATE: 2002-12-13

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1386

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 496

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-712-425-496

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
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Db 1 GYW 3

RESULT 7

US-10-712-425-525  
; Sequence 525, Application US/10712425  
; Publication No. US20040180380A1  
; GENERAL INFORMATION:

; APPLICANT: LEE, FRANK D.

; APPLICANT: MENG, XUN

; APPLICANT: LIVINGSTON, DAVID

; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN

; TITLE OF INVENTION: MODIFICATION ANALYSIS

; FILE REFERENCE: ENGE-P02-001

; CURRENT APPLICATION NUMBER: US/10/712,425

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/379,626

; PRIOR FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: 60/393,137

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,197

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,211

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,223

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,233

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,235

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,280

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/430,948

; PRIOR FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 60/433,319

; PRIOR FILING DATE: 2002-12-13

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1386

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 525

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-712-425-525

Query Match 61.5%; Score 24; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
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Db 2 GYW 4

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US-10-418-943-48  
; Sequence 48, Application US/10418943  
; Publication No. US20040002441A1  
; GENERAL INFORMATION:

; APPLICANT: Segall, Anca

; APPLICANT: Pinilla, Clemencia

; TITLE OF INVENTION: RECOMBINATION MODULATORS AND METHODS

; TITLE OF INVENTION: FOR PRODUCING AND USING THE SAME

; FILE REFERENCE: 011443 008-999

; CURRENT APPLICATION NUMBER: US/10/418,943

; CURRENT FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: 09/602,087

; PRIOR FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 48

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-418-943-48

Query Match 61.5%; Score 24; DB 15; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXW 7  
||| |  
Db 1 YWCYWW 6

RESULT 9  
US-10-346-737A-45  
; Sequence 45, Application US/10346737A  
; Publication No. US20040142379A1  
; GENERAL INFORMATION:  
; APPLICANT: St. Hilaire, Phaedria  
; TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS  
; FILE REFERENCE: 11225.16US01  
; CURRENT APPLICATION NUMBER: US/10/346,737A  
; CURRENT FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-10-346-737A-45

Query Match 61.5%; Score 24; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 4 GYW 6

RESULT 10  
US-09-884-767A-38  
; Sequence 38, Application US/09884767A  
; Publication No. US20020192789A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX Corp.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Luneau, Christopher J.  
; APPLICANT: Ladner, Robert C  
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
; CURRENT APPLICATION NUMBER: US/09/884,767A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 09/597,321  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
US-09-884-767A-38

Query Match 61.5%; Score 24; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 1 GYW 3

RESULT 11  
US-09-563-222-53  
; Sequence 53, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-53

Query Match 61.5%; Score 24; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 2 GYW 4

RESULT 12  
US-10-403-938-27  
; Sequence 27, Application US/10403938  
; Publication No. US20040025195A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,  
; TITLE OF INVENTION: BGS-19  
; FILE REFERENCE: D0227 NP  
; CURRENT APPLICATION NUMBER: US/10/403,938  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368,422  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-938-27

Query Match 61.5%; Score 24; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 3 GYW 5

RESULT 13  
US-10-475-853-6  
; Sequence 6, Application US/10475853  
; Publication No. US20040121442A1  
; GENERAL INFORMATION:  
; APPLICANT: Chet, Ilan  
; APPLICANT: Viterbo, Ada  
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING  
; TITLE OF INVENTION: PROMOTERS OF SAME AND USES THEREOF  
; FILE REFERENCE: 27049  
; CURRENT APPLICATION NUMBER: US/10/475,853  
; CURRENT FILING DATE: 2003-11-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide derived from chit36
US-10-475-853-6

Query Match      61.5%; Score 24; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYW 3
      |||
Db      1 GYW 3

RESULT 14
US-10-783-950-53
; Sequence 53, Application US/10783950
; Publication NO. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-950-53

Query Match      61.5%; Score 24; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYW 3
      |||
Db      2 GYW 4

RESULT 15
US-09-852-870A-5
; Sequence 5, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge

US-09-852-870A-5
Query Match      61.5%; Score 24; DB 9; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.5e+06;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YWXXXW 7
      :|
Db      3 FWKTSW 8

Search completed: December 29, 2004, 22:39:08
Job time : 141 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:13:51 ; Search time 38 Seconds  
(without alignments)  
20.256 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYWXWWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	51.3	5	2 JH0253	gut pentapeptide -
2	15	38.5	6	2 PT0532	T-cell receptor be
3	14	35.9	6	2 B35640	cerebellar degener
4	14	35.9	6	2 PT0629	T-cell receptor be
5	14	35.9	7	2 S21230	dermorphin (Trp-4,
6	14	35.9	7	2 PT0728	T-cell receptor be
7	14	35.9	7	2 S33567	tubulin beta-3 cha
8	13	33.3	4	2 S09478	globulin IV alpha
9	13	33.3	6	2 A61411	ameletin - rat
10	13	33.3	7	1 A61324	dermorphin - Rohde
11	13	33.3	7	2 A60139	fatty-acid synthas
12	13	33.3	7	2 S71870	glutathione transf
13	13	33.3	7	2 S36662	dermorphin (lys-7)
14	13	33.3	8	2 PH1618	Ig H chain V-D-J r
15	12	30.8	8	2 JS0315	leucokinin V - Mad
16	11	28.2	3	3 F37196	bradykinin-potenti
17	11	28.2	4	2 A34626	RPCH-related neuro
18	11	28.2	4	2 B53284	T-cell receptor be
19	11	28.2	4	2 PT0661	T-cell receptor be
20	11	28.2	5	2 A32516	cholecystokinin-5
21	11	28.2	5	2 A60803	neuropeptide - sea
22	11	28.2	5	2 PT0281	Ig heavy chain CRD
23	11	28.2	5	2 PT0308	Ig heavy chain CRD
24	11	28.2	5	2 PT0729	T-cell receptor be
25	11	28.2	5	2 PT0580	T-cell receptor be
26	11	28.2	5	2 G37196	bradykinin-potenti
27	11	28.2	6	2 S66195	alcohol dehydrogen
28	11	28.2	6	2 B34835	dnaA protein - Pse
29	11	28.2	6	2 A31263	dihydrofolate redu

30	11	28.2	6	2 B31263	dihydrofolate redu
31	11	28.2	6	2 PT0519	T-cell receptor be
32	11	28.2	6	2 PT0637	T-cell receptor be
33	11	28.2	6	2 PT0641	T-cell receptor be
34	11	28.2	6	2 PT0726	T-cell receptor be
35	11	28.2	6	2 F41946	T-cell receptor ga
36	11	28.2	6	2 PD0028	pev-kinin 2 - pena
37	11	28.2	6	2 A61068	locustakinin - mig
38	11	28.2	6	4 I79564	hypothetical TCL3
39	11	28.2	7	2 S09652	hypothetical prote
40	11	28.2	7	2 PQ0727	H2 class I protein
41	11	28.2	7	2 E48394	glycoprotein compo
42	11	28.2	7	2 PH1602	Ig H chain V-D-J r
43	11	28.2	7	2 PT0526	T-cell receptor be
44	11	28.2	7	2 PT0628	T-cell receptor be
45	11	28.2	7	2 PT0642	T-cell receptor be

ALIGNMENTS

RESULT 1

JH0253  
gut pentapeptide - Japanese eel  
C;Species: Anguilla japonica (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755  
A;Accession: JH0253  
A;Molecule type: protein  
A;Residues: 1-5 <UES>  
A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric, and of the circular muscle of the gastro-intestinal junction.

Query Match 51.3%; Score 20; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3

Db 1 GFW 3

RESULT 2

PT0532  
T-cell receptor beta chain V-D-J region (100-4AJ) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0532  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0532  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: adult thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 38.5%; Score 15; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYW 3

Db 4 GYW 6



RESULT 3  
B35640  
cerebellar degeneration-related protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 24-Jun-1993  
C;Accession: B35640  
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990  
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker  
A;Reference number: A35640; MUID:90222173; PMID:2326268  
A;Accession: B35640  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-6 <CHE>  
  
Query Match 35.9%; Score 14; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YW 3  
:|  
Db 1 FW 2  
  
RESULT 4  
PT0629  
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0629; PT0528  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0629  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH  
A;Accession: PT0528  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FE2>  
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB  
C;Keywords: T-cell receptor  
  
Query Match 35.9%; Score 14; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
| |  
Db 3 GDW 5  
  
RESULT 5  
S21230  
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
C;Accession: S21230  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S21230  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
  
Query Match 35.9%; Score 14; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YW 3  
:|  
Db 3 FW 4  
  
RESULT 6  
PT0728  
T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0728  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0728  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor  
  
Query Match 35.9%; Score 14; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYW 3  
| |  
Db 3 GDW 5  
  
RESULT 7  
S33567  
tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)  
C;Species: Drosophila melanogaster  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C;Accession: S33567  
R;Hinz, U.; Wolk, A.; Renkawitz-Pohl, R.  
Development 116, 543-554, 1992  
A;Title: Ultrabithorax is a regulator of beta-3 tubulin expression in the Drosophila vis  
A;Reference number: S33567; MUID:93170162; PMID:1363225  
A;Accession: S33567  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <HIN>  
A;Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g437744E  
C;Genetics:  
A;Gene: FlyBase:beta-Tub60D  
A;Cross-references: FlyBase:FBgn0003888  
A;Introns: 5/3  
  
Query Match 35.9%; Score 14; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YW 3  
:|  
Db 6 FW 7  
  
RESULT 8  
S09478  
globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)  
N;Alternate names: 11S globulin alpha subunit gamma chain  
C;Species: Cucurbita sp. (cucurbit)  
C;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 08-Nov-1996  
C;Accession: S09478  
R;Ohmiya, M.; Hara, I.; Matsubara, H.  
Plant Cell Physiol. 21, 157-167, 1980  
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and t  
A;Reference number: S09066

A;Accession: S09478  
A;Molecule type: protein  
A;Residues: 1-4 <OHM>

Query Match 33.3%; Score 13; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 3 GY 4

RESULT 9  
A61411  
ameletin - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C;Accession: A61411  
R;Burzynski, S.R.  
Anal. Biochem. 70, 359-365, 1976  
A;Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the  
A;Reference number: A61411; MUID:76182447; PMID:1267130  
A;Accession: A61411  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <BUR>  
C;Superfamily: unassigned animal peptides  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 13; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 3 GY 4

RESULT 10  
A61324  
dermorphin - Rohde's leaf frog  
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C;Date: 17-Jul-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C;Accession: A61324  
R;Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.  
Int. J. Pept. Protein Res. 17, 316-321, 1981  
A;Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz  
A;Reference number: A61324; MUID:82029915; PMID:7287302  
A;Accession: A61324  
A;Molecule type: protein  
A;Residues: 1-7 <MON>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
C;Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin  
F;2/Modified site: D-alanine (Ala) #status experimental  
F;6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F;7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 33.3%; Score 13; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 4 GY 5

RESULT 11  
A60139  
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 26-May-2000

C;Accession: A60139  
R;Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.  
Biochim. Biophys. Acta 828, 380-382, 1985  
A;Title: Amino acid sequence around the reactive serine residue of the thioesterase domain  
A;Reference number: A60139; MUID:85175165; PMID:3921056  
A;Accession: A60139  
A;Molecule type: protein  
A;Residues: 1-7 <HAR>  
C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homol  
ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-n  
C;Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enz  
F;5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 33.3%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 3 GY 4

RESULT 12  
S71870  
glutathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)  
N;Alternate names: glutathione S-transferase class mu 9  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 07-May-1999  
C;Accession: S71870  
R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.  
Biochem. J. 317, 879-884, 1996  
A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray  
A;Reference number: S71864; MUID:96332484; PMID:8760377  
A;Accession: S71870  
A;Molecule type: protein  
A;Residues: 1-7 <ROU>  
C;Comment: At least five species-independent classes of cytosolic glutathion transferases  
s mitochondrial form are known.  
C;Complex: dimer  
C;Function:  
A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v  
A;Pathway: detoxification; xenobiotics metabolism  
A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism  
es of damage  
C;Superfamily: glutathione transferase  
C;Keywords: acetylated amino end; blocked amino end; dimer; transferase  
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 33.3%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
||  
Db 5 GY 6

RESULT 13  
S36662  
dermorphin (Lys-7) [validated] - two-colored leaf frog  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 10-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
C;Accession: S36662  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S36662  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 33.3%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
Db 4 GY 5

RESULT 14

PH1618  
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1618  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1618  
A;Molecule type: DNA  
A;Residues: 1-8 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
Db 5 GY 6

RESULT 15

JS0315  
leucokinin V - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: JS0315  
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 27-30, 1987  
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
A;Reference number: JS0315  
A;Accession: JS0315  
A;Molecule type: protein  
A;Residues: 1-8 <HOL>  
A;Cross-references: UNIPROT:P19987  
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act  
C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.8%; Score 12; DB 2; Length 8;  
Best Local Similarity 28.6%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GYXXXW 7  
Db 1 GSGFSSW 7

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:09:06 ; Search time 185 Seconds  
(without alignments)  
24.881 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYXXXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 835

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	51.3	8	2	Q62721 rattus norv
2	20	51.3	8	2	Aab333374 homo sapi
3	19	48.7	5	1	P38639 mus musculi
4	16	41.0	7	2	Q9BRY4 homo sapien
5	15	38.5	4	1	P58649 octopus min
6	15	38.5	8	2	Q64971 alfalfa mos
7	13	33.3	8	1	ALL5 CYDPO
8	13	33.3	8	2	O02831
9	13	33.3	8	2	Q95213
10	13	33.3	8	2	Q70Y57
11	13	33.3	8	2	Q70Y84
12	13	33.3	8	2	Q6LDP8
13	13	33.3	8	2	Q9R5R2
14	13	33.3	8	2	CAD45500 plectrant
15	13	33.3	8	2	CAD45547 fuerstia
16	13	33.3	8	2	AAA26011
17	13	33.3	8	2	AAA26012
18	12	30.8	8	1	LCK5 LEUMA
19	12	30.8	8	1	PK4 PERAM
20	11	28.2	2	1	GWA_SEPOF
21	11	28.2	5	1	BPP7 BOTIN
22	11	28.2	6	1	E101_LITRU
23	11	28.2	6	1	LOK1_LOCMI
24	11	28.2	7	1	BRHP_CONIM
25	11	28.2	7	1	TPFY_PACDA
26	11	28.2	7	1	TY51_LITRU
27	11	28.2	7	1	WWA1_ACHFUF
28	11	28.2	7	1	WWA2_ACHFUF
29	11	28.2	7	1	WWA3_ACHFUF
30	11	28.2	7	2	Q95945
31	11	28.2	7	2	O49223 glycine max

32	11	28.2	7	2	Q8GL00	Q8g100 borrelia bu
33	11	28.2	7	2	Q8GL04	Q8g104 borrelia bu
34	11	28.2	7	2	Q8KMS9	Q8kms9 enterobacte
35	11	28.2	7	2	Q8JE81	Q8je81 human immun
36	11	28.2	8	1	ACI_THUAL	P18691 thunnus alb
37	11	28.2	8	1	AKHG_GRYBI	P14086 gryllus bim
38	11	28.2	8	1	AKH_LIBAU	P25418 libellula a
39	11	28.2	8	1	AKH_MELML	P25423 melolontha
40	11	28.2	8	1	AKH_PROTE	P61856 protophormi
41	11	28.2	8	1	AKH_TABAT	P14595 tabanus atr
42	11	28.2	8	1	CI25_CYPDO	P83661 cyphononyx
43	11	28.2	8	1	CKKN_MACEU	P30369 macropus eu
44	11	28.2	8	1	COW2_CONPU	P58785 conus purpu
45	11	28.2	8	1	HTF1_PERAM	P04548 periplaneta

ALIGNMENTS

RESULT 1

Q62721 ID Q62721 PRELIMINARY; PRT; 8 AA.  
AC Q62721;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TremBLrel. 08, Last annotation update)  
DE Prohibitin (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Fisher;  
RX MEDLINE=95331633; PubMed=7607556;  
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,  
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,  
RA McClung J.K.;  
RT "Regions of evolutionary conservation between the rat and human  
prohibitin-encoding genes.";  
RL Gene 158:291-294(1995).  
DR EMBL; U17178; AAA86692.1; -.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 51.3%; Score 20; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 WXXXW 7  
Db 2 WRSEW 6

RESULT 2

AAB333374 ID AAB333374 PRELIMINARY; PRT; 8 AA.  
AC AAB333374;  
DT 02-MAR-2004 (TremBLrel. 27, Created)  
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)  
DE Collagen alpha 5(IV) chain (Fragment).  
GN COL4A5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95156893; PubMed=7853788;  
RA Nakazato H., Hattori S., Ushijima T., Matsuura T., Koitabashi Y.,  
RA Takada T., Yoshioka K., Endo F., Matsuda I.;  
RT "Mutations in the COL4A5 gene in Alport syndrome: a possible mutation



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RT in primordial germ cells.";
RL Kidney Int. 46:1307-1314(1994).
DR EMBL; S75903; AAB33374.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 933 MW; 7370437735BAB378 CRC64;

Query Match 51.3%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WXXXW 7
| |
Db 2 WDSLW 6

RESULT 3
UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=9500907;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 48.7%; Score 19; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WXXXW 7
| |
Db 1 WIGRW 5

RESULT 4
Q9BRY4 PRELIMINARY; PRT; 7 AA.
ID Q9BRY4
AC Q9BRY4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SQSTM1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005857; AAH05857.3; -.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0019901; F:protein kinase binding; ISS.
DR GO; GO:0042169; F:SH2 domain binding; ISS.
DR GO; GO:0043130; F:ubiquitin binding; ISS.
DR GO; GO:0016197; P:endosome transport; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0045944; P:positive regulation of transcription from P. . .; ISS.
DR GO; GO:0008104; P:protein localization; ISS.
DR GO; GO:0043122; P:regulation of I-kappaB kinase/NF-kappaB cas. . .; ISS.
DR GO; GO:0006950; P:response to stress; ISS.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR000433; Znf_ZZ.
DR Pfam; PF00569; ZZ; 1.
DR SMART; SM00165; UBA; 1.
DR SMART; SM00291; Znf_ZZ; 1.
DR PROSITE; PS00303; UBA; 1.
DR PROSITE; PS01357; ZF_ZZ_1; UNKNOWN_1.
DR PROSITE; PS0135; ZF_ZZ_2; 1.
SQ SEQUENCE 7 AA; 779 MW; 737728769DDDD6F0 CRC64;

Query Match 41.0%; Score 16; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3
| |
Db 5 GLW 7

RESULT 5
OCP3_OCTMI STANDARD; PRT; 4 AA.
ID OCP3_OCTMI
AC P58649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less active
CC than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
```



CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
KW D-amino acid; Direct protein sequencing; Hormone.  
FT MOD\_RES 2 D-serine (in form Ocp-4).  
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 38.5%; Score 15; DB 1; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
| |  
Db 1 GSW 3

RESULT 6

Q64971 PRELIMINARY; PRT; 8 AA.  
ID Q64971  
AC Q64971;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Putative ORF (Fragment).  
OS Alfalfa mosaic virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Alfamovirus.  
OX NCBI\_TaxID=12321;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81124289; PubMed=6927843;  
RA Koper-Zwarthoff E.C., Brederode F.T.M., Veeneman G., van Boom J.H.,  
RA Bol J.F.;  
RT "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus  
RT RNAs and the intercistronic junction in RNA 3."  
RL Nucleic Acids Res. 8:5635-5647(1980).  
DR EMBL; V00047; CAA23416.1; --  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 917 MW; 69D40B0775A365B8 CRC64;

Query Match 38.5%; Score 15; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
| |  
Db 1 GSW 3

RESULT 7

ALL5 CYDPO STANDARD; PRT; 8 AA.  
ID ALL5\_CYDPO  
AC P82156;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cydiastatin 5.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily."  
RL Peptides 18:1301-1309(1997).  
CC -1- SIMILARITY: Belongs to the allatostatin family.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 8 Leucine amide.  
SQ SEQUENCE 8 AA; 898 MW; 922879CABB58640D CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
| |  
Db 3 GY 4

RESULT 8

O02831 PRELIMINARY; PRT; 8 AA.  
AC O02831;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Pro alpha 1 type III collagen protein (Fragment).  
GN Name=pro alpha 1 type III collagen;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96377339; PubMed=8783186;  
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,  
RA Vuorio E.;  
RT "Evidence for insufficient chondrocytic differentiation during repair  
RT of full-thickness defects of articular cartilage."  
RL Matrix Biol. 15:39-47(1996).  
DR EMBL; S83371; AAD14433.1; --  
KW Collagen.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YW 3  
: |  
Db 1 HW 2

RESULT 9

Q95213 PRELIMINARY; PRT; 8 AA.  
ID Q95213  
AC Q95213;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Df (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F-I/rgm;  
RX MEDLINE=97315886; PubMed=9171891;  
RA Chen H.T., Alexander C.B., Chen F.F., Mage R.G.;  
RT "Rabbit DQ52 and DH gene expression in early B-cell development."  
RL Mol. Immunol. 33:1313-1321(1996).  
DR EMBL; U62585; AAB18735.1; --  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 845 MW; 5CA861B5AB58677B CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2



QY 1 GY 2  
||  
Db 4 GY 5

QY 1 GY 2  
||  
Db 5 GY 6

Search completed: December 29, 2004, 22:27:08  
Job time : 186 secs

RESULT 14  
CAD45500  
ID CAD45500 PRELIMINARY; PRT; 8 AA.  
AC CAD45500;  
DT 14-MAR-2004 (TrEMBLrel. 27, Created)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Ribosomal protein (Fragment).  
GN RPS16.  
OS Plectranthus buchananii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.  
OX NCBI\_TaxID=204181;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,  
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;  
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)  
RT based on three plastid DNA regions.";  
RL Mol. Phylogenet. Evol. 31:277-299(2004).  
DR EMBL; AJ505379; CAD45500.1; --  
KW Chloroplast; Ribosomal protein.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 945 MW; 6EA415A5BEAB5863 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
Db 2 GY 3

RESULT 15  
CAD45547  
ID CAD45547 PRELIMINARY; PRT; 8 AA.  
AC CAD45547;  
DT 14-MAR-2004 (TrEMBLrel. 27, Created)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Ribosomal protein (Fragment).  
GN RPS16.  
OS Fuerstia africana.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.  
OX NCBI\_TaxID=204226;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,  
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;  
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)  
RT based on three plastid DNA regions.";  
RL Mol. Phylogenet. Evol. 31:277-299(2004).  
DR EMBL; AJ505427; CAD45547.1; --  
KW Chloroplast; Ribosomal protein.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 55.6981 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYXXXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	10	4	AAB99759 Rhesus D
2	34	87.2	12	4	AAB99769 Rhesus D
3	34	87.2	452	4	AAU03644 Group B S
4	34	87.2	466	6	ABU21589 Protein e
5	34	87.2	472	6	ABU38334 Protein e
6	34	87.2	474	6	ABU24881 Protein e
7	34	87.2	475	5	ABP30560 Streptoco
8	34	87.2	475	6	ABU40245 Protein e
9	34	87.2	475	6	ABU29756 Protein e
10	34	87.2	478	7	ADC97241 E. faeciu
11	34	87.2	479	5	ABP26968 Streptoco
12	34	87.2	490	5	ABB55389 Lactococc
13	34	87.2	496	5	ABB55385 Lactococc
14	34	87.2	499	7	ABO74582 Pseudomon
15	34	87.2	506	6	ABU22414 Protein e
16	34	87.2	585	7	ADA49403 Multi-epi
17	34	87.2	585	8	ADO24081 Epigene c
18	34	87.2	865	7	ABO70593 Pseudomon
19	33	84.6	10	5	ABP53931 VEGFR-3 b
20	33	84.6	10	5	ABP53932 VEGFR-3 b
21	33	84.6	69	4	AAO13595 Human pol
22	33	84.6	116	2	AAR15437 Heavy cha
23	33	84.6	116	6	ABO27261 ICAM-1 bi
24	33	84.6	116	6	ABO27269 ICAM-1 bi
25	33	84.6	116	6	ABO27263 ICAM-1 bi

26	33	84.6	116	6	ABO27259	Abo27259 ICAM-1 bi
27	33	84.6	116	6	ABO27255	Abo27255 ICAM-1 bi
28	33	84.6	116	6	ABO27277	Abo27277 Humanised
29	33	84.6	116	6	ABO27273	Abo27273 Murine 1A
30	33	84.6	116	6	ABO27257	Abo27257 ICAM-1 bi
31	33	84.6	116	6	ABO27271	Abo27271 ICAM-1 bi
32	33	84.6	116	6	ABO27267	Abo27267 ICAM-1 bi
33	33	84.6	117	6	ABO27265	Abo27265 ICAM-1 bi
34	33	84.6	118	7	ADJ95639	Adj95639 Insulin-1
35	33	84.6	119	8	ADL11890	Adl11890 CDR trans
36	33	84.6	119	8	ADL11886	Adl11886 Chimera a
37	33	84.6	120	4	AAB62747	Aab62747 Human HIV
38	33	84.6	137	7	ADJ95626	Adj95626 Rat insul
39	33	84.6	138	3	AAY77591	Aay77591 Anti-huma
40	33	84.6	138	3	AAY77595	Aay77595 Anti-huma
41	33	84.6	138	4	AAB78864	Aab78864 Anti-huma
42	33	84.6	138	4	AAB78860	Aab78860 Anti-huma
43	33	84.6	163	7	ABM73967	Abm73967 DNA clone
44	33	84.6	227	6	ABU36339	Abu36339 Protein e
45	33	84.6	240	2	AAR15443	Aar15443 Single ch

ALIGNMENTS

RESULT 1  
AAB99759  
ID AAB99759 standard; peptide; 10 AA.  
XX  
AC AAB99759;  
XX  
DT 21-SEP-2001 (first entry)  
XX  
DE Rhesus D antibody binding peptide SEQ ID NO:4.  
XX

Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
prophylaxis; haemolytic disease of the newborn; HDN; ITP;  
idiopathic thrombocytopaenic purpura; immunoglobulin.

Homo sapiens.  
XX  
PN EP1106625-A1.  
XX

PD 13-JUN-2001.

XX PF 17-NOV-1999; 99EP-00122858.

XX PR 17-NOV-1999; 99EP-00122858.

XX PA (ZLBB-) ZLBB BIOPLASMA AG.

XX PI Miescher S, Hofmann A, Fisch I;

XX XX WPI; 2001-383568/41.

XX Novel peptides capable of binding Rhesus D antibodies are used to  
PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the  
PT newborn (HDN).

XX PS Claim 1; Page 12; 19pp; English.

XX The present sequence represents a peptide capable of binding Rhesus D  
CC antibodies (I). Also described in the present invention are: (1) a  
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
CC (II) operably linked to an expression control system; (3) a cell (IV)  
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
CC peptides having immunologic properties of Rhesus D protein epitopes  
CC comprising subjecting an antibody/antibody fragment recognising an  
CC epitope of Rhesus D protein to several panning rounds with a phage  
CC display library, and identifying immunogenic peptide sequences which are  
CC mimotopes which differ in their amino acid sequence from the amino acid



CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
CC with foreign erythrocytes thereby avoiding the risk of transmission of  
CC viral diseases like AIDS and hepatitis B  
XX  
SQ Sequence 10 AA;  
  
Query Match 87.2%; Score 34; DB 4; Length 10;  
Best Local Similarity 57.1%; Pred. No. 9.9;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXW 7  
Db 1 GYWSAKW 7  
  
RESULT 2  
AAB99769  
ID AAB99769 standard; peptide; 12 AA.  
XX  
AC AAB99769;  
XX  
DT 21-SEP-2001 (first entry)  
XX  
DE Rhesus D antibody related peptide #5.  
XX  
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;  
KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 1. .12  
XX  
PN EP1106625-A1.  
XX  
PD 13-JUN-2001.  
XX  
PF 17-NOV-1999; 99EP-00122858.  
XX  
PR 17-NOV-1999; 99EP-00122858.  
XX  
PA (ZLBB-) ZLB BIOPLASMA AG.  
XX  
PI Miescher S, Hofmann A, Fisch I;  
XX  
WPI; 2001-383568/41.  
DR  
XX  
PT Novel peptides capable of binding Rhesus D antibodies are used to  
PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the  
PT newborn (HDN).  
XX  
PS Example 1; Page 8; 19pp; English.  
XX  
CC The present invention describes peptides capable of binding Rhesus D  
CC antibodies (I). Also described in the present invention are: (1) a  
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
CC (II) operably linked to an expression control system; (3) a cell (IV)  
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
CC peptides having immunologic properties of Rhesus D protein epitopes  
CC comprising subjecting an antibody/antibody fragment recognising an  
CC epitope of Rhesus D protein to several panning rounds with a phage  
CC display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid  
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
CC with foreign erythrocytes thereby avoiding the risk of transmission of  
CC viral diseases like AIDS and hepatitis B. The present sequence represents  
CC an anti-Rhesus D (RhD) antibody related peptide which is used in an  
CC example from the present invention  
XX  
SQ Sequence 12 AA;  
  
Query Match 87.2%; Score 34; DB 4; Length 12;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXW 7  
Db 2 GYWSAKW 8  
  
RESULT 3  
AAU03644  
ID AAU03644 standard; protein; 452 AA.  
XX  
AC AAU03644;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Group B Streptococcus antigenic protein, ID-119.  
XX  
KW Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;  
KW meningitis; neonate; antigenic; vaccine; infection; genital tract;  
KW capsid polysaccharide vaccination.  
XX  
OS Streptococcus agalactiae.  
XX  
PN WO200132882-A2.  
XX  
PD 10-MAY-2001.  
XX  
PF 07-SEP-2000; 2000WO-GB003437.  
XX  
PR 07-SEP-1999; 99GB-00021125.  
XX  
PA (MICR-) MICROBIAL TECHNIKS LTD.  
XX  
PI Le Page RWF, Wells JM, Hanniffy SB;  
XX  
WPI; 2001-316444/33.  
DR N-PSDB; AAS07061.  
XX  
PT New polypeptides derived from Streptococcus agalactiae are useful to  
PT provide detection of, and vaccination against, Group B Streptococcus  
PT infections, particularly to prevent infection in neonates.  
XX  
PS Claim 1; Fig 1; 178pp; English.  
XX  
CC AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus  
CC agalactiae) amino acid sequences of the invention. S. agalactiae is an  
CC encapsulated bacterium which is a major pathogen of humans causing sepsis  
CC and meningitis in neonates as well as adults. The S. agalactiae antigenic  
CC polypeptides are used to vaccinate against Group B Streptococcus  
CC infections, particularly to prevent infection in new born children  
CC arising from the maternal genital tract. An immunogenic composition is  
CC useful in the preparation of a medicament for the treatment or  
CC prophylaxis of Group B Streptococcus infection. The invention does not  
CC have the disadvantages of varied response rate associated with prior art  
CC capsid polysaccharide vaccination against Group B Streptococcus

XX SQ Sequence 452 AA;  
Query Match 87.2%; Score 34; DB 4; Length 452;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
Db 92 GYWLSAW 98  
RESULT 4  
ABU21589  
ID ABU21589 standard; protein; 466 AA.  
XX AC ABU21589;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #7116.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Burkholderia fungorum.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA25459.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 49513; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 466 AA;  
Query Match 87.2%; Score 34; DB 6; Length 466;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
Db 86 GYWVSAW 92  
RESULT 5  
ABU38334  
ID ABU38334 standard; protein; 472 AA.  
XX AC ABU38334;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #23861.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Pseudomonas aeruginosa.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA42204.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 66258; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 472 AA;

Query Match 87.2%; Score 34; DB 6; Length 472;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
||| |  
Db 94 GYWISAW 100

RESULT 6  
ABU24881  
ID ABU24881 standard; protein; 474 AA.  
XX  
AC ABU24881;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #10408.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Clostridium botulinum.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA28751.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 52805; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 474 AA;

Query Match 87.2%; Score 34; DB 6; Length 474;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
||| |  
Db 95 GYWLSAW 101

RESULT 7  
ABP30560  
ID ABP30560 standard; protein; 475 AA.  
XX  
AC ABP30560;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 10296.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus agalactiae.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB004789.  
XX  
PR 27-OCT-2000; 2000GB-00026333.  
PR 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-00005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;  
PI Tettelin H;



XX WPI; 2002-352536/38.  
DR N-PSDB; ABN71191.  
XX  
PT New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX  
PS Claim 1; Page 4161; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN711526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 475 AA;  
Query Match 87.2%; Score 34; DB 5; Length 475;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
Db 92 GYWLAW 98  
RESULT 8  
ABU40245  
ID ABU40245 standard; protein; 475 AA.  
XX  
AC ABU40245;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #25772.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Pseudomonas putida.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA44115.  
XX

PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 68169; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 475 AA;  
Query Match 87.2%; Score 34; DB 6; Length 475;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
Db 93 GYWISAW 99  
RESULT 9  
ABU29756  
ID ABU29756 standard; protein; 475 AA.  
XX  
AC ABU29756;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #15283.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Enterococcus faecium.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA33626.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 57680; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 475 AA;  
  
Query Match 87.2%; Score 34; DB 6; Length 475;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db |||||  
95 GYWLSAW 101  
  
RESULT 10  
ADC97241  
ID ADC97241 standard; protein; 478 AA.  
XX  
AC ADC97241;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE *E. faecium* protein sequence SEQ ID 6868.  
XX  
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;  
KW abdominal-pelvic infection.  
XX  
OS Enterococcus faecium.

XX US6583275-B1.  
PN  
XX 24-JUN-2003.  
PD  
XX 30-JUN-1998; 98US-00107532.  
PF  
XX 02-JUL-1997; 97US-0051571P.  
PR 14-MAY-1998; 98US-0085598P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-799836/75.  
DR N-PSDB; ADC93587.  
XX  
PT New isolated nucleic acid derived from *Enterococcus faecium* encoding an  
PT *Enterococcus faecium* polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.  
XX  
PS Example 1; SEQ ID NO 6868; 243pp; English.  
XX  
CC The invention relates to an isolated nucleic acid derived from  
CC *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcription regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids is useful for diagnosing pathological conditions  
CC resulting from *E. faecium* bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of *Candida albicans* -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating *Enterococcus faecium* infections. The present sequence represents  
CC one if the disclosed *E. faecium* proteins.  
XX  
SQ Sequence 478 AA;  
  
Query Match 87.2%; Score 34; DB 7; Length 478;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db |||||  
98 GYWLSAW 104  
  
RESULT 11  
ABP26968  
ID ABP26968 standard; protein; 479 AA.  
XX  
AC ABP26968;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 3112.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus agalactiae.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.



XX 29-OCT-2001; 2001WO-GB004789.  
PF 27-OCT-2000; 2000GB-00026333.  
XX 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-00005640.  
XX (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX Telford J, Massignani V, Margarit Y Rosl, Grandi G, Fraser C;  
PI Tettelin H;  
XX WPI; 2002-352536/38.  
DR N-PSDB; ABN67599.  
XX New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX Claim 1; Page 3464; 4525pp; English.  
XX The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 479 AA;  
Query Match 87.2%; Score 34; DB 5; Length 479;  
Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
Db 96 GYWLSAW 102  
RESULT 12  
ABB55389  
ID ABB55389 standard; protein; 490 AA.  
XX  
AC ABB55389;  
XX 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX Lactococcus lactis protein arcD1.  
DE Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX Lactococcus lactis; IL1403.  
XX FR2807446-A1.  
PN 12-OCT-2001.  
XX  
PD 11-APR-2000; 2000FR-00004630.  
XX  
PF 11-APR-2000; 2000FR-00004630.  
XX  
PR 11-APR-2000; 2000FR-00004630.

XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
PA Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
XX WPI; 2002-043418/06.  
XX New nucleotide sequence useful in the identification or Lactococcus  
PT lactis and related species.  
XX Claim 6; SEQ ID NO 2091; 2504pp; French.  
XX The present invention is related to a Lactococcus lactis nucleotide  
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
CC acid sequence is useful in the detection and/or amplification of nucleic  
CC acid sequence, particularly to identify Lactococcus lactis or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO200177334 (published 18-OCT-2001) which is available in  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX Sequence 490 AA;  
SQ Query Match 87.2%; Score 34; DB 5; Length 490;  
Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
Db 93 GYWLSAW 99  
RESULT 13  
ABB55385  
ID ABB55385 standard; protein; 496 AA.  
XX  
AC ABB55385;  
XX 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX Lactococcus lactis protein arcD2.  
DE Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX Lactococcus lactis; IL1403.  
XX FR2807446-A1.  
PN 12-OCT-2001.  
XX  
PD 11-APR-2000; 2000FR-00004630.  
XX  
PF 11-APR-2000; 2000FR-00004630.  
XX  
PR 11-APR-2000; 2000FR-00004630.  
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
PA Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
XX WPI; 2002-043418/06.  
XX New nucleotide sequence useful in the identification or Lactococcus  
PT lactis and related species.  
XX Claim 6; SEQ ID NO 2087; 2504pp; French.  
XX The present invention is related to a Lactococcus lactis nucleotide  
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
CC acid sequence is useful in the detection and/or amplification of nucleic

CC acid sequence, particularly to identify Lactococcus lactis or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO200177334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 496 AA;

Query Match 87.2%; Score 34; DB 5; Length 496;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 93 GYWISAW 99

RESULT 14  
ABO74582  
ID ABO74582 standard; protein; 499 AA.

XX ABO74582;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #6757.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

PD 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR N-PSDB; ABD08153.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 23328; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC segdata.uspto.gov/sequence.html

XX

SQ Sequence 499 AA;

Query Match 87.2%; Score 34; DB 7; Length 499;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 111 GYWISAW 117

RESULT 15  
ABU22414  
ID ABU22414 standard; protein; 506 AA.

XX ABU22414;

DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #7941.

DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia mallei.

XX WO200277183-A2.

PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA26284.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 50338; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 506 AA;

Query Match 87.2%; Score 34; DB 6; Length 506;  
Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GYVXXXW 7  
||| |  
Db 124 GYWISAW 130

Search completed: December 30, 2004, 13:07:56  
Job time : 55.6981 secs

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QM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 18.4151 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYWXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	478	4 US-09-107-532A-6868	Sequence 6868, Ap
2	34	87.2	499	4 US-09-252-991A-23328	Sequence 23328, A
3	34	87.2	865	4 US-09-252-991A-19339	Sequence 19339, A
4	33	84.6	543	4 US-09-252-991A-18697	Sequence 18697, A
5	33	84.6	1498	4 US-09-792-616-9	Sequence 9, Appli
6	33	84.6	1503	4 US-09-792-616-3	Sequence 3, Appli
7	32	82.1	177	4 US-09-543-681A-7620	Sequence 7620, Ap
8	32	82.1	252	3 US-09-502-653-10	Sequence 10, Appl
9	32	82.1	263	4 US-09-610-906-12	Sequence 12, Appl
10	32	82.1	274	4 US-09-248-796A-15791	Sequence 15791, A
11	32	82.1	278	4 US-09-145-828A-11	Sequence 11, Appl
12	32	82.1	278	4 US-09-903-456-18	Sequence 18, Appl
13	32	82.1	339	4 US-09-252-991A-26841	Sequence 26841, A
14	32	82.1	362	1 US-08-415-751-6	Sequence 6, Appli
15	32	82.1	367	4 US-09-248-796A-15188	Sequence 15188, A
16	32	82.1	492	4 US-09-107-532A-6945	Sequence 6945, Ap
17	32	82.1	500	4 US-09-252-991A-21214	Sequence 21214, A
18	31	79.5	342	4 US-09-252-991A-32031	Sequence 32031, A
19	30	76.9	11	4 US-09-069-827A-87	Sequence 87, Appl
20	30	76.9	16	4 US-09-620-091-81	Sequence 81, Appl
21	30	76.9	519	4 US-09-198-452A-479	Sequence 479, App
22	30	76.9	654	4 US-09-252-991A-18441	Sequence 18441, A
23	29	74.4	34	4 US-09-270-767-60715	Sequence 60715, A
24	29	74.4	35	3 US-09-082-279B-1191	Sequence 1191, Ap
25	29	74.4	35	3 US-09-315-304B-1191	Sequence 1191, Ap
26	29	74.4	35	4 US-09-834-784-1191	Sequence 1191, Ap
27	29	74.4	35	4 US-09-515-965A-1191	Sequence 1191, Ap

28	29	74.4	35	4 US-09-350-641C-1191	Sequence 1191, Ap
29	29	74.4	35	4 US-09-350-841A-1191	Sequence 1191, Ap
30	29	74.4	55	4 US-09-621-976-7633	Sequence 7633, Ap
31	29	74.4	69	4 US-09-621-976-7239	Sequence 7239, Ap
32	29	74.4	139	4 US-09-252-991A-19685	Sequence 19685, A
33	29	74.4	142	4 US-09-252-991A-22994	Sequence 22994, A
34	29	74.4	197	4 US-09-543-681A-5312	Sequence 5312, Ap
35	29	74.4	227	4 US-09-489-039A-8752	Sequence 8752, Ap
36	29	74.4	255	4 US-09-270-767-45223	Sequence 45223, A
37	29	74.4	625	4 US-09-252-991A-28537	Sequence 28537, A
38	29	74.4	930	4 US-09-198-452A-470	Sequence 470, App
39	28	71.8	19	4 US-09-794-529B-8	Sequence 8, Appli
40	28	71.8	19	4 US-09-794-517A-8	Sequence 8, Appli
41	28	71.8	19	4 US-09-011-645E-8	Sequence 8, Appli
42	28	71.8	19	4 US-09-794-832-8	Sequence 8, Appli
43	28	71.8	19	4 US-09-680-806A-8	Sequence 8, Appli
44	28	71.8	19	4 US-09-552-868-8	Sequence 8, Appli
45	28	71.8	19	4 US-09-636-295-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-107-532A-6868  
; Sequence 6868, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6868:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 478 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...478  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:  
US-09-107-532A-6868



Query Match 87.2%; Score 34; DB 4; Length 478;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
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Db 98 GYWLAW 104

RESULT 2  
US-09-252-991A-23328  
; Sequence 23328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23328  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23328

Query Match 87.2%; Score 34; DB 4; Length 499;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 111 GYWISAW 117

RESULT 3  
US-09-252-991A-19339  
; Sequence 19339, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19339  
; LENGTH: 865  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19339

Query Match 87.2%; Score 34; DB 4; Length 865;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 487 GYWISAW 493

RESULT 4

US-09-252-991A-18697  
; Sequence 18697, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18697  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18697

Query Match 84.6%; Score 33; DB 4; Length 543;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 331 GYWMVSW 337

RESULT 5  
US-09-792-616-9  
; Sequence 9, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-792-616-9

Query Match 84.6%; Score 33; DB 4; Length 1498;  
Best Local Similarity 57.1%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
||| |  
Db 960 GYWLW 966

RESULT 6  
US-09-792-616-3  
; Sequence 3, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      84.6%; Score 33; DB 4; Length 1503;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
Db      965 GYWLSLW 971

RESULT 7
US-09-543-681A-7620
; Sequence 7620, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7620
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7620

Query Match      82.1%; Score 32; DB 4; Length 177;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
Db      43 GYWINW 49

RESULT 8
US-09-502-653-10
; Sequence 10, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schlein, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481.200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Bacillus circulans
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US-09-502-653-10

Query Match      82.1%; Score 32; DB 3; Length 252;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
Db      210 GYWEPAW 216

RESULT 9
US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Klinger, Tod M.
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT
; FILE REFERENCE: PC-0012 CIP
; CURRENT APPLICATION NUMBER: US/09/610,906
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 09/226,994
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. 6566066: g2346968
; PUBLICATION INFORMATION:
US-09-610-906-12

Query Match      82.1%; Score 32; DB 4; Length 263;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
Db      224 GYWDFHW 230

RESULT 10
US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15791
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791

Query Match      82.1%; Score 32; DB 4; Length 274;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
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Db      84 GYWPITW 90
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RESULT 11
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      82.1%; Score 32; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
|||||
Db      108 GYWIFLW 114

RESULT 12
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match      82.1%; Score 32; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      108 GYWIFLW 114
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RESULT 13
US-09-252-991A-26841
; Sequence 26841, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26841
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26841

Query Match      82.1%; Score 32; DB 4; Length 339;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      261 GYWGYYW 267

RESULT 14
US-08-415-751-6
; Sequence 6, Application US/08415751
; Patent No. 5643772
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-
; TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, DNA
; TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID
; TITLE OF INVENTION: VECTOR AND TRANSFORMED HOST AND
; TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS AND KIT
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILLIPS, MOORE, LEMPJO & FINLEY
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,751
; FILING DATE: 03-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/071,880
; FILING DATE: June 1, 1993
; APPLICATION NUMBER: 07/891,301
; FILING DATE: May 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana Dolezalova
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-1677  
TELEFAX: (415) 324-1678  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 362 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE: Cryptosporidium parvum  
FEATURE:  
NAME/KEY: Positions coded by nonsense codons are  
NAME/KEY: identified as Xaa.  
US-08-415-751-6

Query Match 82.1%; Score 32; DB 1; Length 362;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 216 GYWLTW 222

RESULT 15  
US-09-248-796A-15188  
Sequence 15188, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 15188  
LENGTH: 367  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-15188

Query Match 82.1%; Score 32; DB 4; Length 367;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 276 GYWLVDW 282

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Perfect score: 39  
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Scoring table: BLOSUM62  
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15: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	58	17 US-10-425-115-308836	Sequence 308836,
2	34	87.2	72	16 US-10-437-963-176036	Sequence 176036,
3	34	87.2	452	14 US-10-091-007-88	Sequence 88, Appl
4	34	87.2	466	15 US-10-282-122A-49513	Sequence 49513, A
5	34	87.2	469	14 US-10-369-493-23291	Sequence 23291, A
6	34	87.2	472	15 US-10-282-122A-66258	Sequence 66258, A
7	34	87.2	474	15 US-10-282-122A-52805	Sequence 52805, A
8	34	87.2	475	14 US-10-369-493-13733	Sequence 13733, A
9	34	87.2	475	15 US-10-282-122A-57680	Sequence 57680, A
10	34	87.2	475	15 US-10-282-122A-68169	Sequence 68169, A
11	34	87.2	506	15 US-10-282-122A-50338	Sequence 50338, A
12	34	87.2	585	9 US-09-894-018-87	Sequence 87, Appl
13	34	87.2	585	17 US-10-474-960A-87	Sequence 87, Appl

14	33	84.6	10	13	US-10-046-922-34	Sequence 34, Appl
15	33	84.6	10	13	US-10-046-922-35	Sequence 35, Appl
16	33	84.6	47	17	US-10-425-115-287762	Sequence 287762,
17	33	84.6	104	17	US-10-425-115-273234	Sequence 273234,
18	33	84.6	116	10	US-09-910-483-1	Sequence 1, Appli
19	33	84.6	116	10	US-09-910-483-5	Sequence 5, Appli
20	33	84.6	116	10	US-09-910-483-9	Sequence 9, Appli
21	33	84.6	116	10	US-09-910-483-13	Sequence 13, Appl
22	33	84.6	116	10	US-09-910-483-17	Sequence 17, Appl
23	33	84.6	116	10	US-09-910-483-21	Sequence 21, Appl
24	33	84.6	116	10	US-09-910-483-25	Sequence 25, Appl
25	33	84.6	116	10	US-09-910-483-29	Sequence 29, Appl
26	33	84.6	116	10	US-09-910-483-33	Sequence 33, Appl
27	33	84.6	116	10	US-09-910-483-37	Sequence 37, Appl
28	33	84.6	116	10	US-09-910-483-41	Sequence 41, Appl
29	33	84.6	116	10	US-09-910-483-43	Sequence 43, Appl
30	33	84.6	129	17	US-10-425-115-357518	Sequence 357518,
31	33	84.6	138	14	US-10-160-232-86	Sequence 86, Appl
32	33	84.6	138	14	US-10-160-232-90	Sequence 90, Appl
33	33	84.6	227	15	US-10-282-122A-64263	Sequence 64263, A
34	33	84.6	229	17	US-10-425-115-344695	Sequence 344695,
35	33	84.6	296	14	US-10-156-761-9632	Sequence 9632, Ap
36	33	84.6	296	14	US-10-369-493-19811	Sequence 19811, A
37	33	84.6	466	14	US-10-369-493-16537	Sequence 16537, A
38	33	84.6	467	16	US-10-437-963-199114	Sequence 199114,
39	33	84.6	516	16	US-10-450-022-7	Sequence 7, Appli
40	33	84.6	526	16	US-10-450-022-4	Sequence 4, Appli
41	33	84.6	526	16	US-10-450-022-5	Sequence 5, Appli
42	33	84.6	526	17	US-10-433-747B-2	Sequence 2, Appli
43	33	84.6	526	17	US-10-433-747B-17	Sequence 17, Appl
44	33	84.6	526	17	US-10-450-185B-2	Sequence 2, Appli
45	33	84.6	526	17	US-10-450-185B-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-425-115-308836  
; Sequence 308836, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 308836  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_44726C.1.pep  
US-10-425-115-308836

Query Match 87.2%; Score 34; DB 17; Length 58;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXXXW 7  
|||  
Db 49 GYWGASW 55  
RESULT 2  
US-10-437-963-176036  
; Sequence 176036, Application US/10437963  
; Publication No. US20040123343A1

```

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176036
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
US-10-437-963-176036

Query Match      87.2%; Score 34; DB 16; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXW 7
      |||
Db      34 GYWSSW 40

RESULT 3
US-10-091-007-88
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited
; APPLICANT: Le Page, Richard W F Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88

Query Match      87.2%; Score 34; DB 14; Length 452;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXW 7
      |||
Db      92 GYWLAW 98

RESULT 4
US-10-282-122A-49513
; Sequence 49513, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
```

```

; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49513
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49513

Query Match      87.2%; Score 34; DB 15; Length 466;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXW 7
      |||
Db      86 GYWVSAW 92

RESULT 5
US-10-369-493-23291
; Sequence 23291, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23291
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Query Match 87.2%; Score 34; DB 14; Length 469;  
Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
| | | | |  
Db 97 GYVWASW 103

RESULT 6

US-10-282-122A-66258  
; Sequence 66258, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66258  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-66258  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66258  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

Query Match 87.2%; Score 34; DB 15; Length 472;  
Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
| | | | |  
Db 94 GYWISAW 100

RESULT 7

US-10-282-122A-52805  
; Sequence 52805, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52805  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Clostridium botulinum

US-10-282-122A-52805  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 13733

Query Match 87.2%; Score 34; DB 15; Length 474;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
| | | | |  
Db 95 GYWLSAW 101

RESULT 8

US-10-369-493-13733  
; Sequence 13733, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 13733

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; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13733

Query Match      87.2%; Score 34; DB 14; Length 475;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GYWXXXW 7
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Db      93 GYWISAW 99
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RESULT 9
US-10-282-122A-57680
; Sequence 57680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57680
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Enterococcus faecium
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US-10-282-122A-57680

Query Match      87.2%; Score 34; DB 15; Length 475;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GYWXXXW 7
      |||||
Db      95 GYWLAW 101
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RESULT 10
US-10-282-122A-68169
; Sequence 68169, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68169
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida
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US-10-282-122A-68169
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Query Match      87.2%; Score 34; DB 15; Length 475;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GYWXXXW 7
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Db      93 GYWISAW 99
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RESULT 11
US-10-282-122A-50338
; Sequence 50338, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
```



```
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50338
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50338
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Query Match      87.2%; Score 34; DB 15; Length 506;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GYWXXXW 7
      |||||
Db      124 GYWISAW 130
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RESULT 12
US-09-894-018-87
; Sequence 87, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
US-09-894-018-87

Query Match      87.2%; Score 34; DB 9; Length 585;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
      |||||
Db      22 GYWQATW 28
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RESULT 13
US-10-474-960A-87
; Sequence 87, Application US/10474960A
; Publication No. US20040248113A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denise
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
; TITLE OF INVENTION: Acid Constructs and Peptides Encoded Thereby
; FILE REFERENCE: 2060.0320004
; CURRENT APPLICATION NUMBER: US/10/474,960A
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/US02/09877
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/894,018
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
US-10-474-960A-87
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Query Match      87.2%; Score 34; DB 17; Length 585;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GYWXXXW 7
      |||||
Db      22 GYWQATW 28
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RESULT 14
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match      84.6%; Score 33; DB 13; Length 10;
Best Local Similarity 57.1%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      2 GYWLTIW 8
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RESULT 15
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
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Query Match      84.6%; Score 33; DB 13; Length 10;
Best Local Similarity 57.1%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||
Db      2 GYWLTIW 8
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Search completed: December 30, 2004, 13:50:03  
Job time : 60.6226 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 9.20755 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYWXXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	72	2 T03190	hypothetical prote
2	34	87.2	108	2 S12193	hypothetical prote
3	34	87.2	345	2 T37139	hypothetical prote
4	34	87.2	469	2 D70048	ABC transporter (a
5	34	87.2	472	2 E83497	probable amino aci
6	34	87.2	475	2 T46745	arginine/ornithine
7	34	87.2	482	2 JH0110	arginine/ornithine
8	34	87.2	490	2 C86879	arginine/ornitine
9	34	87.2	497	2 G86878	arginine/ornitine
10	33	84.6	142	2 C34903	Ig heavy chain pre
11	33	84.6	227	2 S73905	CDPdiacylglycerol-
12	33	84.6	250	2 A69843	hypothetical prote
13	33	84.6	289	2 G72215	oligopeptide ABC t
14	33	84.6	360	2 AE2047	hypothetical prote
15	33	84.6	441	2 C95307	probable transport
16	33	84.6	508	2 C95282	probable ABC trans
17	33	84.6	517	2 AI3201	hypothetical prote
18	33	84.6	519	2 E83268	probable carbohydr
19	33	84.6	534	2 T15414	hypothetical prote
20	33	84.6	535	2 B95952	probable dipeptide
21	33	84.6	541	2 AC2392	hypothetical prote
22	33	84.6	563	2 AH2975	hypothetical prote
23	33	84.6	563	2 C98307	opha protein limpo
24	33	84.6	592	2 T15413	hypothetical prote
25	33	84.6	778	2 T31037	hypothetical prote
26	33	84.6	1502	2 T42216	multidrug resistan
27	32	82.1	71	2 S22905	lysis protein S -
28	32	82.1	83	2 E69903	hypothetical prote
29	32	82.1	187	2 G83047	hypothetical prote

ALIGNMENTS

RESULT 1

T03190

hypothetical protein 72B - rice mitochondrion  
C;Species: mitochondrion Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: T03190

R;Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.  
Plant Cell Physiol. 35, 1239-1244, 1994

A;Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existence  
A;Reference number: Z14841; MUID:95211382; PMID:7545979

A;Accession: T03190

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-72 <ITA>

A;Cross-references: UNIPROT:Q35302; EMBL:D32052; NID:g769704; PIDN:BAA06811.1; PID:g769704  
A;Experimental source: cultivar Nipponbare

C;Genetics:

A;Genome: mitochondrion

C;Keywords: mitochondrion

Query Match 87.2%; Score 34; DB 2; Length 72;  
Best Local Similarity 57.1%; Pred. No. 15;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
||| |  
Db 34 GYWSSHW 40

RESULT 2

S12193

hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1  
C;Species: Thiobacillus ferrooxidans

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S12193

R;Drolet, M.; Zanga, P.; Lau, P.C.K.

Mol. Microbiol. 4, 1381-1391, 1990

A;Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans  
A;Reference number: S12188; MUID:91125140; PMID:2280689

A;Accession: S12193

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-108 <DRO>

A;Cross-references: UNIPROT:P20088; EMBL:X52699; NID:g48158; PIDN:CAA36930.1; PID:g48164  
C;Genetics:

A;Genome: plasmid pTF1

Query Match 87.2%; Score 34; DB 2; Length 108;  
Best Local Similarity 57.1%; Pred. No. 21;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

Db	89 GYWRSSW 95	
RESULT 3		
T37139	hypothetical protein SCJ9A.03c - Streptomyces coelicolor	
C;Species:	Streptomyces coelicolor	
C;Date:	03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004	
C;Accession:	T37139	
R;Harris, D.;	Bentley, S.D.;	Parkhill, J.;
	Barrell, B.G.;	Rajandream, M.A.
	submitted to the EMBL Data Library, August 1999	
A;Reference number:	221622	
A;Accession:	T37139	
A;Status:	preliminary; translated from GB/EMBL/DDBJ	
A;Molecule type:	DNA	
A;Residues:	1-345 <HAR>	
A;Cross-references:	UNIPROT:Q9S1R7; EMBL:AL109972; PIDN:CAB53264.1; GSPDB:GN00070; SCOE	
A;Experimental source:	strain A3(2)	
C;Genetics:		
A;Gene:	SCOEDB:SCJ9A.03c	
C;Superfamily:	Streptomyces coelicolor hypothetical protein SCJ9A.03c	
Query Match	87.2%;	Score 34; DB 2; Length 345;
Best Local Similarity	57.1%;	Pred. No. 61;
Matches	4; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7	
Db	147 GYWAARW 153	
RESULT 4		
D70048	ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis	
C;Species:	Bacillus subtilis	
C;Date:	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004	
C;Accession:	D70048	
R;Kunst, F.;	Ogasawara, N.;	Moszer, I.;
	Albertini, A.M.;	Alloni, G.;
	Azevedo, V.;	Bertex
	C.;	Bron, S.;
	Brouillet, S.;	Bruschi, C.V.;
	Caldwell, B.;	Capuano, V.;
	Carter, N.M.;	Cho
	A.;	Ehrlich, S.D.;
	Emmerson, P.T.;	Entian, K.D.;
	Errington, J.;	Fabret, C.;
	Ferrari, E.	
	Nature 390, 249-256, 1997	
A;Authors:	Foulger, D.;	Fritz, C.;
	Fujita, M.;	Fujita, Y.;
	Fuma, S.;	Galizzi, A.;
	Galler	
	iech, J.;	Harwood, C.R.;
	Henaut, H.;	Holsappel, S.;
	Hosono, S.;	Hullo, M.F.
	Koetter, P.;	Koningstein, G.;
	Krogh, S.;	Kumano, M.;
	Kurita, K.;	Lapidus, A.;
	Lardinois,	
	A;Authors:	Lauber, J.;
	Lazarevic, V.;	Lee, S.M.;
	Levine, A.;	Liu, H.;
	Masuda, S.;	Maueel
	Y, M.;	Ogawa, K.;
	Ogiwara, A.;	Oudega, B.;
	Park, S.H.;	Parro, V.;
	Pohl, T.M.;	Portetelle
	Rieger, M.;	Rivolta, C.;
	Rocha, E.;	Roche, B.;
	Rose, M.;	Sadaie, Y.;
	Sato, T.;	Scanlon,
	A;Authors:	Schleich, S.;
	Schroeter, R.;	Scoffone, F.;
	Sekiguchi, J.;	Sekowska, A.;
	Seror	
	akeuchi, M.;	Tamakoshi, A.;
	Tanaka, T.;	Terpstra, P.;
	Tognoni, A.;	Tosato, V.;
	Uchiyama,	
	T.;	Winters, P.;
	Wipat, A.;	Yamamoto, H.;
	Yamane, K.;	Yasumoto, K.;
	Yata, K.;	Yoshida, K
	A;Authors:	Yoshikawa, H.F.;
	Zumstein, E.;	Yoshikawa, H.;
	Danchin, A.	
A;Title:	The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.	
A;Reference number:	A69580; MUID:98044033; PMID:9384377	
A;Accession:	D70048	
A;Status:	preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type:	DNA	
A;Residues:	1-469 <KUN>	
A;Cross-references:	UNIPROT:O32204; GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15339.	
A;Experimental source:	strain 168	
C;Genetics:		
A;Gene:	yvsh	
C;Superfamily:	L-lysine transport protein	
Query Match	87.2%;	Score 34; DB 2; Length 469;
Best Local Similarity	57.1%;	Pred. No. 80;
Matches	4; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7	
Db	97 GYWVASW 103	

RESULT 5		
E83497	probable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PAO1)	
C;Species:	Pseudomonas aeruginosa	
C;Date:	15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004	
C;Accession:	E83497	
R;Stover, C.K.;	Pham, X.Q.;	Erwin, A.L.;
	Mizoguchi, S.D.;	Warrener, P.;
	Hickey, M.J.;	Br
	adman, S.;	Yuan, Y.;
	Brody, L.L.;	Coulter, S.N.;
	Folger, K.R.;	Kas, A.;
	Larbig, K.;	Lim,
	.;	Lory, S.;
	Olson, M.V.	
	Nature 406, 959-964, 2000	
A;Title:	Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen	
A;Reference number:	A82950; MUID:20437337; PMID:10984043	
A;Accession:	E83497	
A;Status:	preliminary	
A;Molecule type:	DNA	
A;Residues:	1-472 <STO>	
A;Cross-references:	UNIPROT:Q9I4E4; GB:AE004549; GB:AE004091; NID:g9947110; PIDN:AAG0458;	
A;Experimental source:	Strain PAO1	
C;Genetics:		
A;Gene:	PA1194	
C;Superfamily:	L-lysine transport protein	
Query Match	87.2%;	Score 34; DB 2; Length 472;
Best Local Similarity	57.1%;	Pred. No. 81;
Matches	4; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7	
Db	94 GYWISAW 100	
RESULT 6		
T46745	arginine/ornithine antiporter [imported] - Lactobacillus sakei	
C;Species:	Lactobacillus sakei	
C;Date:	20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004	
C;Accession:	T46745	
R;Zuniga, M.;	Championier-Verges, M.C.;	Perez-Martinez, G.;
	Zagorec, M.;	Perez-Martinez, C
	J. Bacteriol. 180, 4154-4159, 1998	
A;Title:	Structural and functional analysis of the gene cluster encoding the enzymes of t	
A;Reference number:	Z23141; MUID:98361904; PMID:9696763	
A;Accession:	T46745	
A;Status:	preliminary; translated from GB/EMBL/DDBJ	
A;Molecule type:	DNA	
A;Residues:	1-475 <ZUN>	
A;Cross-references:	UNIPROT:O53092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:g2;	
C;Genetics:		
A;Gene:	arcd	
C;Function:		
A;Description:	necessary for arginine transport; involved in ornithine-arginine exchange	
A;Pathway:	arginine catabolism	
C;Superfamily:	L-lysine transport protein	
Query Match	87.2%;	Score 34; DB 2; Length 475;
Best Local Similarity	57.1%;	Pred. No. 81;
Matches	4; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7	
Db	94 GYWLSAW 100	
RESULT 7		
JH0110	arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa	
C;Species:	Pseudomonas aeruginosa	
C;Date:	31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004	
C;Accession:	JH0110; A82999	
R;Luethi, E.;	Baur, H.;	Gamper, M.;
	Brunner, F.;	Villeva, D.;
	Mercenier, A.;	Haas, D.
	Gene 87, 37-43, 1990	
A;Title:	The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cont	
A;Reference number:	JH0110; MUID:90236296; PMID:2158926	
A;Accession:	JH0110	

A;Molecule type: DNA  
A;Residues: 1-482 <LJE>  
A;Cross-references: UNIPROT:P18275; GB:M33223; NID:g151030; PIDN:AAA25719.1; PID:g151031  
A;Experimental source: strain PA01  
A;Note: the gene encoding this protein is located upstream of the arcABC genes which encode for the synthesis of L-lysine  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brumfield, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: A82999  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-482 <STO>  
A;Cross-references: GB:AE004930; GB:AE004091; NID:g9951472; PIDN:AAG08555.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: arcD; PA5170  
C;Superfamily: L-lysine transport protein  
C;Keywords: transmembrane protein  
  
Query Match 87.2%; Score 34; DB 2; Length 482;  
Best Local Similarity 57.1%; Pred. No. 82;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
||| |  
Db 94 GYWISAW 100  
  
RESULT 8  
C86879  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: C86879  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, S.; Artigues, C.; et al.  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: C86879  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-490 <STO>  
A;Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:GN001  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: arcD1  
C;Superfamily: L-lysine transport protein  
  
Query Match 87.2%; Score 34; DB 2; Length 490;  
Best Local Similarity 57.1%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
||| |  
Db 93 GYWL SAW 99  
  
RESULT 9  
G86878  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: G86878  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, S.; Artigues, C.; et al.  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: G86878  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-497 <STO>  
A;Cross-references: UNIPROT:Q9CE19; GB:AE005176; PID:g12725079; PIDN:AAK06129.1; GSPDB:GN001  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: arcD2  
C;Superfamily: L-lysine transport protein  
  
Query Match 87.2%; Score 34; DB 2; Length 497;  
Best Local Similarity 57.1%; Pred. No. 85;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
||| |  
Db 93 GYWISAW 99  
  
RESULT 10  
C34903  
Ig heavy chain precursor V region (5-27) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
C;Accession: C34903  
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive antibodies  
A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: C34903  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-142 <BED>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-119/Domain: immunoglobulin homology <IMM>  
  
Query Match 84.6%; Score 33; DB 2; Length 142;  
Best Local Similarity 57.1%; Pred. No. 40;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
||| |  
Db 126 GYWFAYW 132  
  
RESULT 11  
S73905  
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) pgsA - Mycobacterium tuberculosis  
N;Alternate names: hypothetical protein A65\_orf227  
C;Species: Mycoplasma pneumoniae  
A;Variety: ATCC 29342  
C;Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S73905  
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
A;Reference number: S73327; MUID:97105885; PMID:8948633  
A;Accession: S73905  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-227 <HIM>  
A;Cross-references: UNIPROT:P75520; EMBL:AE000057; GB:U00089; NID:g1674279; PIDN:AAB9622  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C;Genetics:  
A;Gene: pgsA  
A;Genetic code: SGC3  
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase  
C;Keywords: transferase  
  
Query Match 84.6%; Score 33; DB 2; Length 227;  
Best Local Similarity 57.1%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GYWXXXW 7  
||| |



Db	84 GYWARKW 90
RESULT 12	
A69843	hypothetical protein yjba - Bacillus subtilis
C;Species:	Bacillus subtilis
C;Date:	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession:	A69843
R;Kunst, F.;	Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.;	Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.;	Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature	390, 249-256, 1997
A;Authors:	Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.;	Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.;	Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors:	Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.;	Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.;	Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors:	Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.;	Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.;	Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors:	Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title:	The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference	number: A69580; MUID:98044033; PMID:9384377
A;Accession:	A69843
A;Status:	preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule	type: DNA
A;Residues:	1-250 <KUN>
A;Cross-references:	UNIPROT:O31597; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB12998.
A;Experimental	source: strain 168
C;Genetics:	
A;Gene:	yjba
C;Superfamily:	Bacillus subtilis hypothetical protein yjba
Query Match	84.6%; Score 33; DB 2; Length 250;
Best Local Similarity	57.1%; Pred. No. 68;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 GYWXXXW 7
Db	185 GYWTEW 191
RESULT 13	
G72215	oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species:	Thermotoga maritima
C;Date:	11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession:	G72215
R;Nelson, K.E.;	Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.;	Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.	
Nature	399, 323-329, 1999
A;Title:	Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference	number: A72200; MUID:99287316; PMID:10360571
A;Accession:	G72215
A;Status:	preliminary
A;Molecule	type: DNA
A;Residues:	1-289 <ARN>
A;Cross-references:	UNIPROT:Q9X270; GB:AE001813; GB:AE000512; NID:g4982321; PIDN:AAD3681
A;Experimental	source: strain MSB8
C;Genetics:	
A;Gene:	TM1748
C;Superfamily:	oligopeptide permease protein oppB
Query Match	84.6%; Score 33; DB 2; Length 289;
Best Local Similarity	57.1%; Pred. No. 77;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 GYWXXXW 7
Db	11 GYWKAFW 17

RESULT 14

AE2047	hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)
C;Species:	Nostoc sp. PCC 7120
A;Note:	Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date:	14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession:	AE2047
R;Kaneko, T.;	Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.;	Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res.	8, 205-213, 2001
A;Title:	Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference	number: AB1807; MUID:21595285; PMID:11759840
A;Accession:	AE2047
A;Status:	preliminary
A;Molecule	type: DNA
A;Residues:	1-360 <KUR>
A;Cross-references:	UNIPROT:Q8YVP3; GB:BA000019; PIDN:BA073630.1; PID:g17131021; GSPDB:G
A;Experimental	source: strain PCC 7120
C;Genetics:	
A;Gene:	all1931
Query Match	84.6%; Score 33; DB 2; Length 360;
Best Local Similarity	57.1%; Pred. No. 94;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 GYWXXXW 7
Db	127 GYWSYGW 133
RESULT 15	
C95307	probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) mag
C;Species:	Sinorhizobium meliloti
C;Date:	24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession:	C95307
R;Barnett, M.J.;	Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
.;	Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A.	98, 9883-9888, 2001
A;Title:	Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference	number: A95262; MUID:21396509; PMID:11481432
A;Accession:	C95307
A;Status:	preliminary
A;Molecule	type: DNA
A;Residues:	1-441 <KUR>
A;Cross-references:	UNIPROT:Q92ZT6; GB:AE006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:G
A;Experimental	source: strain 1021, megaplasmid pSymA
R;Galibert, F.;	Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.;	Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.;	Hyman, R.W.; Jones, T.
Science	293, 668-672, 2001
A;Authors:	Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaullt, P.;	Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Title:	The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference	number: A96039; MUID:21368234; PMID:11474104
A;Contents:	annotation
C;Genetics:	
A;Gene:	Sma0684
A;Genome:	plasmid
C;Superfamily:	L-lysine transport protein
Query Match	84.6%; Score 33; DB 2; Length 441;
Best Local Similarity	57.1%; Pred. No. 1.1e+02;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 GYWXXXW 7
Db	92 GYWISIW 98



Job time : 9.37421 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 73.8113 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYWXXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	72	2 Q35302	Q35302 oryza sativ
2	34	87.2	108	1 YML2 THIFE	P20088 thiolbacillu
3	34	87.2	130	2 Q7U395	Q7u395 prochloroco
4	34	87.2	236	2 Q9GWG9	Q9wgw9 human immun
5	34	87.2	253	2 O32816	O32816 lactococcus
6	34	87.2	294	2 Q8ET30	Q8et30 oceanobacil
7	34	87.2	333	2 Q6F6U4	Q6f6u4 acinetobact
8	34	87.2	345	2 Q9S1R7	Q9s1r7 streptomyce
9	34	87.2	459	2 Q9KGV3	Q9kgv3 lactococcus
10	34	87.2	464	2 Q84DL5	Q84dl5 oenococcus
11	34	87.2	465	2 Q6HNI4	Q6hni4 bacillus th
12	34	87.2	465	2 Q6I3F7	Q6i3f7 bacillus an
13	34	87.2	465	2 Q73DL5	Q73dl5 bacillus ce
14	34	87.2	465	2 Q8IH27	Q8ihz7 bacillus ce
15	34	87.2	465	2 Q81V71	Q81v71 bacillus an
16	34	87.2	465	2 AAS39630	Aas39630 bacillus
17	34	87.2	465	2 AAT29732	Aat29732 bacillus
18	34	87.2	469	2 Q6TK71	Q6tk71 streptococc
19	34	87.2	469	2 O32204	O32204 bacillus su
20	34	87.2	469	2 AAR30325	Aar30325 streptoco
21	34	87.2	471	2 Q6HP27	Q6hp27 bacillus th
22	34	87.2	471	2 Q73E85	Q73e85 bacillus ce
23	34	87.2	471	2 Q81IH9	Q81ih9 bacillus ce
24	34	87.2	471	2 AAS39409	Aas39409 bacillus
25	34	87.2	472	2 Q9I4E4	Q9i4e4 pseudomonas
26	34	87.2	473	2 Q7NRJ8	Q7nrj8 chromobacte
27	34	87.2	475	1 ARCD LACSK	O53092 lactobacill
28	34	87.2	475	2 Q88P50	Q88p50 pseudomonas
29	34	87.2	475	2 Q88P51	Q88p51 pseudomonas
30	34	87.2	475	2 Q8DWP9	Q8dwp9 streptococc
31	34	87.2	475	2 Q8E2J7	Q8e2j7 streptococc

32	34	87.2	478	1 ARCD_CLOPE	Q46170 clostridium
33	34	87.2	482	1 ARCD_PSEAE	P18275 pseudomonas
34	34	87.2	490	2 Q9CEI5	Q9cel5 lactococcus
35	34	87.2	497	2 Q9KGV0	Q9kgv0 lactococcus
36	34	87.2	497	2 Q9CE19	Q9cel9 lactococcus
37	34	87.2	526	2 Q9K574	Q9k574 lactococcus
38	34	87.2	879	2 Q7ZJJ7	Q7zjj7 human immun
39	33	84.6	130	2 Q7VBG3	Q7vbg3 prochloroco
40	33	84.6	135	2 Q7TUV7	Q7tuv7 prochloroco
41	33	84.6	160	2 Q6NF17	Q6nf17 corynebacte
42	33	84.6	160	2 CAE50615	Caes0615 corynebac
43	33	84.6	213	2 Q9KY37	Q9ky37 streptomyc
44	33	84.6	224	2 Q8S486	Q8s486 zea mays (m
45	33	84.6	227	1 PGSA_MYCPN	P75520 mycoplasma

ALIGNMENTS

RESULT 1  
Q35302  
ID Q35302 PRELIMINARY; PRT; 72 AA.  
AC Q35302;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
DE ORF72B.  
OS Oryza sativa (japonica cultivar-group).  
OG Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,  
RA Il'in Y.V.;  
RT "Structure of long and short copies of the mobile dispersed gene MDG3  
of Drosophila melanogaster.";  
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95308541; PubMed=7788722;  
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiyura M.,  
RA Hirai A.;  
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is  
transcribed from alternative promoters.";  
RL Curr. Genet. 27:184-189(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95211382; PubMed=7545979;  
RA Itadani H., Wakasugi T., Sugita M., Sugiyura M., Nakazono M., Hirai A.;  
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:  
the existence of many sequences that correspond to parts of  
mitochondrial genes in intergenic regions.";  
RL Plant Cell Physiol. 35:1239-1244(1994).  
DR EMBL; D32052; BAA06811.1; -.  
DR PIR; T03190; T03190.  
DR Gramene; Q35302; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
SQ SEQUENCE 72 AA; 8155 MW; D42DE53BED28432E CRC64;

Query Match 87.2%; Score 34; DB 2; Length 72;  
Best Local Similarity 57.1%; Pred. No. 87;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
| | | |  
Db 34 GYWSHW 40

RESULT 2

```
YML2_THIFE
ID_YML2_THIFE STANDARD; PRT; 108 AA.
AC P20088;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 12.3 kDa protein in mobL 3'region (ORF 4).
OS Thiobacillus ferrooxidans.
OG Plasmid pTF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drolet M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
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CC -----
DR EMBL; X52699; CAA36930.1; -.
DR PIR; S12193; S12193.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;

Query Match 87.2%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
   |||||
DB 89 GYWRSSW 95

RESULT 3
Q7U395 PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible Adenoviral fiber protein (Repeat/shaf.
GN OrderedLocusNames=PM1067;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX57092; CAE19526.1; -.
KW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; EE0F4A997FCA8CD8 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
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Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
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DB 7 GYWT LAW 13

RESULT 4
Q9WGW9 PRELIMINARY; PRT; 236 AA.
ID Q9WGW9
AC Q9WGW9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
RT in perinatal human immunodeficiency virus (HIV) type 1 transmission:
RT the ariel project for the prevention of transmission of HIV from
RT mother to infant.";
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121641; AAD29013.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR010659; RVT_connect.
DR InterPro; IPR010661; RVT_thumb.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 236
SQ SEQUENCE 236 AA; 27062 MW; 24D6BB0409A80BB8 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 236;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
   |||||
DB 129 GYWQATW 135

RESULT 5
O32816 PRELIMINARY; PRT; 253 AA.
ID O32816
AC O32816;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine/ornithine antiporter homolog ArcD (Fragment).
GN Name=arcD;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG1363;
RX MEDLINE=97369814; PubMed=9226255;
RA Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
RT "Characterization of Lactococcus lactis UV-sensitive mutants obtained
RT by ISS1 transposition.";
```

RL J. Bacteriol. 179:4473-4479(1997).  
DR EMBL; U81991; AAC45504.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
KW Transmembrane.  
FT NON\_TER 253 253  
SQ SEQUENCE 253 AA; 26569 MW; 1CB8FAEF6C38FBB1 CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 253;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 93 GYWSAW 99  
  
RESULT 6  
Q8ET30  
ID Q8ET30 PRELIMINARY; PRT; 294 AA.  
AC Q8ET30;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ABC transporter permease.  
GN OrderedLocusNames=OB0434;  
OS Oceanobacillus iheyensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831;  
RX MEDLINE=22220767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments.";  
RL Nucleic Acids Res. 30:3927-3935(2002).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE ABC-3 SUBFAMILY OF INTEGRAL MEMBRANE  
CC PROTEINS.  
DR EMBL; AP004594; BAC12390.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001626; ABC\_3.  
DR Pfam; PF00950; ABC-3; 1.  
KW Complete proteome; Transmembrane; Transport.  
SQ SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 294;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 244 GYWIATW 250  
  
RESULT 7  
Q6F6U4  
ID Q6F6U4 PRELIMINARY; PRT; 333 AA.  
AC Q6F6U4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE putative transporter; putative sodium/bile acid transporter family  
DE protein.  
GN OrderedLocusNames=ACIAD3583;  
OS Acinetobacter sp. (strain ADP1).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=62977;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,  
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,  
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;  
RT "Unique features revealed by the genome sequence of Acinetobacter sp.  
RT ADP1, a versatile and naturally transformation competent bacterium.";  
RL Nucleic Acids Res. 0:0-0(2004).  
DR EMBL; CR543861; CAG70223.1; -.  
DR InterPro; IPR002657; BilAc/Na\_sympoort.  
DR Pfam; PF01758; SBF; 1.  
KW Complete proteome.  
SQ SEQUENCE 333 AA; 36530 MW; 7C887F5127A40682 CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 333;  
Best Local Similarity 57.1%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 252 GYWASRW 258  
  
RESULT 8  
Q9SLR7  
ID Q9SLR7 PRELIMINARY; PRT; 345 AA.  
AC Q9SLR7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein SCO0224.  
GN OrderedLocusNames=SCO0224; ORFNames=SCJ9A.03c;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL939104; CAB53264.1; -.  
DR PIR; T37139; T37139.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 345;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db 147 GYWAARW 153  
  
RESULT 9  
Q9KGV3  
ID Q9KGV3 PRELIMINARY; PRT; 459 AA.  
AC Q9KGV3;



DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ArcD1.  
GN Name=arcD1;  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML3;  
RA Chou L., Weimer B., Xie Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML3;  
RA Chou L.-S., Weimer B., Xie Y.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AF282249; AAF86987.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 459 AA; 49146 MW; 9718F27B7B937242 CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 459;  
Best Local Similarity 57.1%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db |||||  
92 GYWLSAW 98  
  
RESULT 10  
Q84DL5 ID Q84DL5 PRELIMINARY; PRT; 464 AA.  
AC Q84DL5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Arginine/ornithine antiporter ArcD2.  
GN Name=arcD2;  
OS Oenococcus oeni (Leuconostoc oenos).  
OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.  
OX NCBI\_TaxID=1247;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 23279;  
RX MEDLINE=22519090; PubMed=12631210;  
RA Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;  
RT "Molecular characterization of Oenococcus oeni genes encoding proteins involved in arginine transport.";  
RL J. Appl. Microbiol. 94:738-746(2003).  
DR EMBL; AF541253; AAO83382.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 464 AA; 50557 MW; 1C6EE79AFF9F8B84 CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 464;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db |||||  
94 GYWLSSW 100  
  
RESULT 11  
Q6HNI4 ID Q6HNI4 PRELIMINARY; PRT; 465 AA.  
AC Q6HNI4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Probable arginine/ornithine antiporter protein.  
GN Name=arcD; ORFNames=BT9727\_0540;  
OS Bacillus thuringiensis serovar konkukian str. 97-27.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus thuringiensis serovar konkukian.  
OX NCBI\_TaxID=281309;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97-27;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AE017355; AAT62417.1; -.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 465 AA; 50153 MW; 534F038C0A379E04 CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 465;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db |||||  
96 GYWAANW 102  
  
RESULT 12  
Q6I3F7 ID Q6I3F7 PRELIMINARY; PRT; 465 AA.  
AC Q6I3F7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Amino acid permease family protein.  
GN OrderedLocusNames=BAS0596;  
OS Bacillus anthracis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1392;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sterne;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AE017225; AAT52924.1; -.  
DR InterPro; IPR002293; AA/rel\_permeasel.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;  
  
Query Match 87.2%; Score 34; DB 2; Length 465;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXXXW 7  
Db |||||

Db	96 GYWAANW 102	SQ	SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;	Query Match 87.2%; Score 34; DB 2; Length 465; Best Local Similarity 57.1%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT 13		Qy	1 GYWXXXW 7	
Q73DL5		Db	96 GYWAANW 102	
ID	Q73DL5 PRELIMINARY; PRT; 465 AA.	RESULT 15		
AC	Q73DL5;	Q81V71	PRELIMINARY; PRT; 465 AA.	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	AC	Q81V71; Q6KX71;	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DE	Amino acid permease family protein.	DT	01-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
GN	OrderedLocusNames=BCE0697;	DE	Amino acid permease family protein.	
OS	Bacillus cereus (strain ATCC 10987).	GN	OrderedLocusNames=BA0629; ORFNames=GBAA0629;	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OS	Bacillus anthracis.	
OX	NCBI_TaxID=222523;	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
RN	[1]	OX	NCBI_TaxID=1392;	
RP	SEQUENCE FROM N.A.	RN	[1]	
RX	PubMed=14960714;	RP	SEQUENCE FROM N.A.	
RA	Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,	RC	STRAIN=Ames / isolate Porton;	
RA	Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,	RX	MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;	
RA	Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;	RA	Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,	
RT	"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic	RA	Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,	
RT	adaptations and a large plasmid related to Bacillus anthracis pXOI.";	RA	Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,	
RL	Nucleic Acids Res. 32:977-988(2004).	RA	Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,	
DR	EMBL; AE017266; AAS39630.1; -.	RA	DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,	
DR	TIGR; BCE0697; -.	RA	Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,	
DR	InterPro; IPR002293; AA/rel_permeasel.	RA	Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,	
DR	InterPro; IPR004841; Permease_region.	RA	Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niemman W.C.,	
DR	Pfam; PF00324; AA_permease; 1.	RA	Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,	
KW	Complete proteome; Transmembrane; Transport.	RA	Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,	
SQ	SEQUENCE 465 AA; 50193 MW; C18384E10EBC639D CRC64;	RA	Hanna P.C., Kolstoe A.-B., Fraser C.M.;	
Query Match 87.2%; Score 34; DB 2; Length 465; Best Local Similarity 57.1%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		RT	"The genome sequence of Bacillus anthracis Ames and comparison to	
		RT	closely related bacteria.";	
		RL	Nature 423:81-86(2003).	
		RN	[2]	
Qy	1 GYWXXXW 7	RP	SEQUENCE FROM N.A.	
Db	96 GYWAANW 102	RC	STRAIN=Ames / isolate 0581;	
RESULT 14		RA	Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,	
Q81HZ7		RA	Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,	
ID	Q81HZ7 PRELIMINARY; PRT; 465 AA.	RA	Fraser C.M.;	
AC	Q81HZ7;	RT	"Bacillus anthracis comparative genomics.";	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	DR	EMBL; AE017026; AAP24646.1; -.	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	DR	EMBL; AE017334; AAT29732.1; -.	
DE	Arginine/ornithine antiporter.	DR	TIGR; BA0629; -.	
GN	ORFNames=BC0629;	DR	GO; GO:0016021; C:integral to membrane; IEA.	
OS	Bacillus cereus (strain ATCC 14579 / DSM 31).	DR	GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	DR	GO; GO:0006865; P:amino acid transport; IEA.	
OX	NCBI_TaxID=226900;	DR	GO; GO:0006810; P:transport; IEA.	
RN	[1]	DR	InterPro; IPR002293; AA/rel_permeasel.	
RP	SEQUENCE FROM N.A.	DR	InterPro; IPR004841; Permease_region.	
RX	MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;	DR	Pfam; PF00324; AA_permease; 1.	
RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,	KW	Transmembrane; Transport.	
RA	Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,	SQ	SEQUENCE 465 AA; 50250 MW; AA04D53505386FA9 CRC64;	
RA	Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,	Query Match 87.2%; Score 34; DB 2; Length 465; Best Local Similarity 57.1%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
RA	Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,	Qy	1 GYWXXXW 7	
RA	Overbeek R., Kyrpides N.C.;	Db	96 GYWAANW 102	
RT	"Genome sequence of Bacillus cereus and comparative analysis with	RESULT 15		
RT	Bacillus anthracis.";	Q81V71	PRELIMINARY; PRT; 465 AA.	
RL	Nature 423:87-91(2003).	AC	Q81V71; Q6KX71;	
DR	EMBL; AE017000; AAP07646.1; -.	DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DR	GO; GO:0016021; C:integral to membrane; IEA.	DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DR	GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.	DT	01-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DR	GO; GO:0006865; P:amino acid transport; IEA.	DE	Amino acid permease family protein.	
DR	GO; GO:0006810; P:transport; IEA.	GN	OrderedLocusNames=BCE0697;	
DR	InterPro; IPR002293; AA/rel_permeasel.	OS	Bacillus cereus (strain ATCC 10987).	
DR	InterPro; IPR004841; Permease_region.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
DR	Pfam; PF00324; AA_permease; 1.	OX	NCBI_TaxID=222523;	
KW	Transmembrane; Transport.	RN	[1]	
		RP	SEQUENCE FROM N.A.	
		RX	PubMed=14960714;	
		RA	Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,	
		RA	Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,	
		RA	Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;	
		RT	"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic	
		RT	adaptations and a large plasmid related to Bacillus anthracis pXOI.";	
		RL	Nucleic Acids Res. 32:977-988(2004).	
		DR	EMBL; AE017266; AAS39630.1; -.	
		DR	TIGR; BCE0697; -.	
		DR	InterPro; IPR002293; AA/rel_permeasel.	
		DR	InterPro; IPR004841; Permease_region.	
		DR	Pfam; PF00324; AA_permease; 1.	
		KW	Complete proteome; Transmembrane; Transport.	
		SQ	SEQUENCE 465 AA; 50193 MW; C18384E10EBC639D CRC64;	
		Query Match 87.2%; Score 34; DB 2; Length 465; Best Local Similarity 57.1%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
		Qy	1 GYWXXXW 7	
		Db	96 GYWAANW 102	
		RESULT 14		
		Q81HZ7	PRELIMINARY; PRT; 465 AA.	
		ID	Q81HZ7	
		AC	Q81HZ7;	
		DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
		DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
		DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
		DE	Arginine/ornithine antiporter.	
		GN	ORFNames=BC0629;	
		OS	Bacillus cereus (strain ATCC 14579 / DSM 31).	
		OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
		OX	NCBI_TaxID=226900;	
		RN	[1]	
		RP	SEQUENCE FROM N.A.	
		RX	MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;	
		RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,	
		RA	Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,	
		RA	Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,	
		RA	Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,	
		RA	Overbeek R., Kyrpides N.C.;	
		RT	"Genome sequence of Bacillus cereus and comparative analysis with	
		RT	Bacillus anthracis.";	
		RL	Nature 423:87-91(2003).	
		DR	EMBL; AE017000; AAP07646.1; -.	
		DR	GO; GO:0016021; C:integral to membrane; IEA.	
		DR	GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.	
		DR	GO; GO:0006865; P:amino acid transport; IEA.	
		DR	GO; GO:0006810; P:transport; IEA.	
		DR	InterPro; IPR002293; AA/rel_permeasel.	
		DR	InterPro; IPR004841; Permease_region.	
		DR	Pfam; PF00324; AA_permease; 1.	
		KW	Transmembrane; Transport.	
		Search completed: December 30, 2004, 13:16:13		
		Job time : 74.8113 secs		



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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:02:29 ; Search time 148 Seconds  
(without alignments)  
19.391 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 153769

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	2	ADD95004 Platelet
2	0	0.0	1	2	ADD94992 Platelet
3	0	0.0	1	2	ADD94993 Platelet
4	0	0.0	1	2	ADD95002 Platelet
5	0	0.0	1	2	ADD94997 Platelet
6	0	0.0	1	2	ADD94999 Platelet
7	0	0.0	1	2	ADD95003 Platelet
8	0	0.0	1	2	ADD94995 Platelet
9	0	0.0	1	2	ADD94998 Platelet
10	0	0.0	1	2	ADD95001 Platelet
11	0	0.0	1	2	ADD94990 Platelet
12	0	0.0	1	2	ADD94991 Platelet
13	0	0.0	1	2	ADD94994 Platelet
14	0	0.0	1	2	ADD94996 Platelet
15	0	0.0	1	2	ADD95000 Platelet
16	0	0.0	1	2	AAY46652 Immunogen
17	0	0.0	1	4	AAM97834 Human pep
18	0	0.0	1	4	AAM97974 Human pep
19	0	0.0	1	4	AAM97643 Human pep
20	0	0.0	1	4	AAM98447 Human pep
21	0	0.0	1	4	AAM98354 Human pep
22	0	0.0	1	4	AAM53290 Human non
23	0	0.0	1	4	AAM53329 Human non
24	0	-0.0	1	4	AAM53291 Human non
25	0	0.0	1	4	AAM53328 Human non

26	0	0.0	1	4	AAM53219	Aam53219 Human non
27	0	0.0	1	4	AAM53218	Aam53218 Human non
28	0	0.0	1	4	AAB91029	Aab91029 Thyrotrop
29	0	0.0	1	4	AAB91739	Aab91739 Opioid pe
30	0	0.0	1	4	AAB92150	Aab92150 Polypepti
31	0	0.0	1	4	AAB91892	Aab91892 Apoptosis
32	0	0.0	1	4	AAB91546	Aab91546 Endotheli
33	0	0.0	1	4	AAB92392	Aab92392 Miscellan
34	0	0.0	1	4	AAB91665	Aab91665 Opioid pe
35	0	0.0	1	4	AAG99966	Aag99966 ERA bindi
36	0	0.0	1	4	AAM00011	Aam00011 ERA bindi
37	0	0.0	1	4	AAG99987	Aag99987 ERA bindi
38	0	0.0	1	4	AAG99983	Aag99983 ERA bindi
39	0	0.0	1	4	AAM00013	Aam00013 ERA bindi
40	0	0.0	1	4	AAM00016	Aam00016 ERA bindi
41	0	0.0	1	4	AAG99988	Aag99988 ERA bindi
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ALIGNMENTS

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DT 29-JAN-2004 (first entry)  
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DE Platelet aggregation inhibitor peptide #146.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
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FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti-platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 11; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;

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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 X 1
Db      1 R 1

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XX
AC ADD94992;
XX
DT 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #134.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
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FH Key Location/Qualifiers
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FT defined)"
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PD 12-JAN-1995.
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PF 22-JUN-1994; 94WO-JP0000999.
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PR 30-JUN-1993; 93JP-00186755.
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XX
PS Disclosure; Page 10; 34pp; Japanese.
XX
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CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ Sequence 1 AA;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 R 1

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ID ADD94993 standard; peptide; 1 AA.
XX
AC ADD94993;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 X 1
Db      1 R 1

RESULT 4
ADD95002
ID ADD95002 standard; peptide; 1 AA.
XX
AC ADD95002;
XX
DT 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #144.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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DT 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #135.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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PN WO9501371-A1.
XX
PD 12-JAN-1995.
XX
PF 22-JUN-1994; 94WO-JP0000999.
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XX
PS Disclosure; Page 10; 34pp; Japanese.
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CC salts. (I) are useful as platelet aggregation inhibitors and are easily
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CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ Sequence 1 AA;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 X 1
Db      1 R 1

RESULT 4
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ID ADD95002 standard; peptide; 1 AA.
XX
AC ADD95002;
XX
DT 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #144.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 7  
ADD95003  
ID ADD95003 standard; peptide; 1 AA.  
XX  
AC ADD95003;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #145.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
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PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 11; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 2; Length 1;  
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 8  
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XX  
AC ADD94995;  
XX  
DT 29-JAN-2004 (first entry)

XX Platelet aggregation inhibitor peptide #137.  
DE  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
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PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
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DR WPI; 1995-060950/08.  
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XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 9  
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AC ADD94998;  
XX  
DT 29-JAN-2004 (first entry)  
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KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX  
PN WO9501371-A1.  
XX

PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 R 1  
  
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AC ADD95001;  
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DT 29-JAN-2004 (first entry)  
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KW platelet aggregation inhibitor; guanidino group; amidino group.  
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DT 29-JAN-2004 (first entry)  
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DE Platelet aggregation inhibitor peptide #143.  
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KW platelet aggregation inhibitor; guanidino group; amidino group.  
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XX  
PR 30-JUN-1993; 93JP-00186755.  
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XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX

PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 R 1  
  
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AC ADD94990;  
XX  
DT 29-JAN-2004 (first entry)  
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XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
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OS Unidentified.  
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PF 22-JUN-1994; 94WO-JP000999.  
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PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
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PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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QY 1 X 1  
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AC ADD94991;  
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KW platelet aggregation inhibitor; guanidino group; amidino group.  
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PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP000999.  
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PR 30-JUN-1993; 93JP-00186755.  
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PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
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DR WPI; 1995-060950/08.  
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XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

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AC ADD94994;  
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DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #136.

XX platelet aggregation inhibitor; guanidino group; amidino group.  
KW Unidentified.  
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FH Key Location/Qualifiers  
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XX  
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XX  
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SQ Sequence 1 AA;

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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

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XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
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OS Unidentified.  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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XX  
PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
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PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
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CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
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QY 1 X 1  
Db 1 R 1  
  
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AC ADD95000;  
XX  
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DE Platelet aggregation inhibitor peptide #142.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
FT defined)"  
XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
PT  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX

CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. NO. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 1 R 1  
  
Search completed: December 29, 2004, 21:18:58  
Job time : 150 secs



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:10:45 ; Search time 36 Seconds  
(without alignments)  
14.737 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 73656

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	0	0.0	1	1	US-07-820-154A-12
2	0	0.0	1	1	US-07-791-213D-24
3	0	0.0	1	1	US-07-791-213D-40
4	0	0.0	1	1	US-08-174-365A-57
5	0	0.0	1	1	US-07-789-913-23
6	0	0.0	1	1	US-07-789-913-25
7	0	0.0	1	1	US-08-049-794-23
8	0	0.0	1	1	US-08-049-794-25
9	0	0.0	1	1	US-08-433-037-12
10	0	0.0	1	1	US-08-448-606-4
11	0	0.0	1	1	US-07-869-933-16
12	0	0.0	1	1	US-08-293-150A-24
13	0	0.0	1	1	US-08-293-150A-40
14	0	0.0	1	1	US-08-496-847-23
15	0	0.0	1	1	US-08-496-847-25
16	0	0.0	1	2	US-08-742-774-23
17	0	0.0	1	2	US-08-742-774-25
18	0	0.0	1	2	US-08-675-354-23
19	0	0.0	1	2	US-08-675-354-25
20	0	0.0	1	2	US-08-097-554A-12
21	0	0.0	1	2	US-08-965-918-23
22	0	0.0	1	2	US-08-965-918-25
23	0	0.0	1	2	US-09-138-439-23
24	0	0.0	1	2	US-09-138-439-25
25	0	0.0	1	3	US-08-480-640A-12
26	0	0.0	1	3	US-08-613-400A-23
27	0	0.0	1	3	US-08-613-400A-25

28	0	0.0	1	3	US-08-801-092-10	Sequence 10, Appl
29	0	0.0	1	3	US-08-801-092-17	Sequence 17, Appl
30	0	0.0	1	3	US-08-801-092-24	Sequence 24, Appl
31	0	0.0	1	3	US-08-801-092-31	Sequence 31, Appl
32	0	0.0	1	3	US-08-801-092-38	Sequence 38, Appl
33	0	0.0	1	3	US-08-801-092-45	Sequence 45, Appl
34	0	0.0	1	3	US-09-298-017-23	Sequence 23, Appl
35	0	0.0	1	3	US-09-298-017-25	Sequence 25, Appl
36	0	0.0	1	3	US-08-295-802-12	Sequence 12, Appl
37	0	0.0	1	3	US-09-392-979A-23	Sequence 23, Appl
38	0	0.0	1	3	US-09-392-979A-25	Sequence 25, Appl
39	0	0.0	1	3	US-09-103-663-16	Sequence 16, Appl
40	0	0.0	1	3	US-08-488-237A-12	Sequence 12, Appl
41	0	0.0	1	3	US-09-117-927-5	Sequence 5, Appli
42	0	0.0	1	3	US-08-375-992A-12	Sequence 12, Appl
43	0	0.0	1	3	US-09-315-113-10	Sequence 10, Appl
44	0	0.0	1	3	US-09-315-113-17	Sequence 17, Appl
45	0	0.0	1	3	US-09-315-113-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-07-820-154A-12  
; Sequence 12, Application US/07820154A  
; Patent No. 5382425  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph.D., Mark D  
; APPLICANT: Junker M.S., David E  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/820,154A  
; FILING DATE: 19920113  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-820-154A-12

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 V 1

RESULT 2  
US-07-791-213D-24

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; Sequence 24, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-24

Query Match      0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 C 1

RESULT 3
US-07-791-213D-40
; Sequence 40, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
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; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-40

Query Match      0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 C 1

RESULT 4
US-08-174-365A-57
; Sequence 57, Application US/08174365A
; Patent No. 5478809
; GENERAL INFORMATION:
; APPLICANT: Seilichi TANIDA et al.
; TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,365A
; FILING DATE: December 28, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 57:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acid  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified site  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note = "Xaa is modified amino acid as  
OTHER INFORMATION: described in specification"  
US-08-174-365A-57

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 X 1

RESULT 5  
US-07-789-913-23  
; Sequence 23, Application US/07789913  
; Patent No. 5559095  
; GENERAL INFORMATION:  
; APPLICANT: Miljanich, George P.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Fox, James A.  
; APPLICANT: Valentino, Karen L.  
; APPLICANT: Bitner, Robert S.  
; APPLICANT: Yamashiro, Donald H.  
; TITLE OF INVENTION: Delayed Treatment Method of Reducing  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/789,913  
FILING DATE: 19911112  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/561,766  
FILING DATE: 02-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/440,094  
FILING DATE: 22-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0005.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 6  
US-07-789-913-25  
; Sequence 25, Application US/07789913  
; Patent No. 5559095  
; GENERAL INFORMATION:  
; APPLICANT: Miljanich, George P.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Fox, James A.  
; APPLICANT: Valentino, Karen L.  
; APPLICANT: Bitner, Robert S.  
; APPLICANT: Yamashiro, Donald H.  
; TITLE OF INVENTION: Delayed Treatment Method of Reducing  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/789,913  
FILING DATE: 19911112  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/561,766  
FILING DATE: 02-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/440,094  
FILING DATE: 22-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0005.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-25

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db1 R 1

RESULT 7  
US-08-049-794-23  
; Sequence 23, Application US/08049794  
; Patent No. 5587454  
; GENERAL INFORMATION:  
; APPLICANT: JUSTICE, ALAN  
; APPLICANT: SINGH, TEJINDER  
; APPLICANT: GOHIL, KISHOR C  
; APPLICANT: VALENTINO, KAREN L  
; APPLICANT: MILJANICH, GEORGE P  
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND  
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/049,794  
; FILING DATE: 19930415  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/814,759  
; FILING DATE: 30-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A.  
; REGISTRATION NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 5865-0009.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE  
; INDIVIDUAL ISOLATE: 32  
US-08-049-794-23

Query Match0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity0.0%; Pred. No. 0;  
Matches0; Conservative0; Mismatches1; Indels0; Gaps0;

QY1 X 1

Db1 R 1

Db1 X 1

RESULT 9  
US-08-433-037-12  
; Sequence 12, Application US/08433037  
; Patent No. 5707828  
; GENERAL INFORMATION:  
; APPLICANT: Sreekrishna, Kotikanyadan  
; APPLICANT: Barr, Kathryn A.  
; APPLICANT: Brierley, Russell A.  
; APPLICANT: Thill, Gregory P.  
; APPLICANT: Tachopp, Juerg F.  
; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN  
; TITLE OF INVENTION: PICHIA PASTORIS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

Query Match0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity0.0%; Pred. No. 0;  
Matches0; Conservative0; Mismatches1; Indels0; Gaps0;

QY1 X 1

Db1 C 1

Db1 C 1

RESULT 8  
US-08-049-794-25  
; Sequence 25, Application US/08049794  
; Patent No. 5587454  
; GENERAL INFORMATION:  
; APPLICANT: JUSTICE, ALAN  
; APPLICANT: SINGH, TEJINDER  
; APPLICANT: GOHIL, KISHOR C  
; APPLICANT: VALENTINO, KAREN L

Query Match0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity0.0%; Pred. No. 0;  
Matches0; Conservative0; Mismatches1; Indels0; Gaps0;

QY1 X 1

Db1 C 1



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/433,037  
FILING DATE: 03-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9108Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-433-037-12

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 L 1

RESULT 10  
US-08-448-606-4  
Sequence 4, Application US/08448606  
Patent No. 572114  
GENERAL INFORMATION:  
APPLICANT: Abrahams n, Lars  
APPLICANT: Holmgren, Erik  
APPLICANT: Kalder n, Christina  
APPLICANT: Lake, Mats  
APPLICANT: Mikaelsson, sa  
APPLICANT: Sejlitz, Torsten  
TITLE OF INVENTION: Expression System For Producing  
TITLE OF INVENTION: Apolipoprotein AI-M  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pollock, Vande Sande & Priddy  
STREET: 1990 M Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,606  
FILING DATE: 25-AUG-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/SE93/01061  
FILING DATE: 11-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Amernick, Burton A.  
REGISTRATION NUMBER: 24,852  
REFERENCE/DOCKET NUMBER: 0151/00121  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)331-7111  
TELEFAX: (202) 293-6229  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acid  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-448-606-4

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Q 1

RESULT 11  
US-07-869-933-16  
Sequence 16, Application US/07869933  
Patent No. 5770396  
GENERAL INFORMATION:  
APPLICANT: KINET, Jean-Pierre  
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
TITLE OF INVENTION: IMMUNOGLOBULIN  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/869,933  
FILING DATE: 19920416  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-869-933-16

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 M 1

RESULT 12  
US-08-293-150A-24  
Sequence 24, Application US/08293150A

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; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-24

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Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 C 1

RESULT 13
US-08-293-150A-40
; Sequence 40, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
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; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-40

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Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 C 1

RESULT 14
US-08-496-847-23
; Sequence 23, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
```

REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0009.31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
US-08-496-847-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 15  
US-08-496-847-25  
Sequence 25, Application US/08496847  
Patent No. 5795864  
GENERAL INFORMATION:  
APPLICANT: Amstutz, Gary A.  
APPLICANT: Bowersox, Stephen S.  
APPLICANT: Gohil, Kishorchandra  
APPLICANT: Adriaenssens, Peter I.  
APPLICANT: Kristipati, Ramasharma  
TITLE OF INVENTION: METHODS AND  
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94306-1546  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/496,847  
FILING DATE: 27-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0009.31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
US-08-496-847-25

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
Db 1 R 1  
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Job time : 37 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:16:31 ; Search time 137 Seconds  
(without alignments)  
21.006 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 83711

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	9	US-09-778-885-5
2	0	0.0	1	9	US-09-909-348-4
3	0	0.0	1	9	US-09-982-172-3
4	0	0.0	1	9	US-09-982-172-4
5	0	0.0	1	9	US-09-982-172-9
6	0	0.0	1	9	US-09-982-172-11
7	0	0.0	1	9	US-09-982-172-19
8	0	0.0	1	9	US-09-982-172-31
9	0	0.0	1	9	US-09-982-172-35
10	0	0.0	1	9	US-09-982-172-37
11	0	0.0	1	9	US-09-982-172-46
12	0	0.0	1	9	US-09-982-172-69
13	0	0.0	1	9	US-09-982-172-80

14	0	0.0	1	9	US-09-982-172-81	Sequence 81, Appl
15	0	0.0	1	9	US-09-982-172-83	Sequence 83, Appl
16	0	0.0	1	9	US-09-982-172-86	Sequence 86, Appl
17	0	0.0	1	9	US-09-982-172-93	Sequence 93, Appl
18	0	0.0	1	9	US-09-982-172-95	Sequence 95, Appl
19	0	0.0	1	9	US-09-982-172-106	Sequence 106, App
20	0	0.0	1	9	US-09-982-172-112	Sequence 112, App
21	0	0.0	1	9	US-09-982-172-120	Sequence 120, App
22	0	0.0	1	9	US-09-982-172-126	Sequence 126, App
23	0	0.0	1	9	US-09-982-172-148	Sequence 148, App
24	0	0.0	1	9	US-09-982-172-149	Sequence 149, App
25	0	0.0	1	9	US-09-982-172-155	Sequence 155, App
26	0	0.0	1	9	US-09-982-172-160	Sequence 160, App
27	0	0.0	1	9	US-09-982-172-172	Sequence 172, App
28	0	0.0	1	9	US-09-982-172-173	Sequence 173, App
29	0	0.0	1	9	US-09-982-172-175	Sequence 175, App
30	0	0.0	1	9	US-09-982-172-189	Sequence 189, App
31	0	0.0	1	9	US-09-982-172-190	Sequence 190, App
32	0	0.0	1	9	US-09-982-172-191	Sequence 191, App
33	0	0.0	1	9	US-09-982-172-195	Sequence 195, App
34	0	0.0	1	9	US-09-982-172-200	Sequence 200, App
35	0	0.0	1	9	US-09-982-172-211	Sequence 211, App
36	0	0.0	1	10	US-09-809-391-395	Sequence 395, App
37	0	0.0	1	10	US-09-809-391-611	Sequence 611, App
38	0	0.0	1	10	US-09-882-171-395	Sequence 395, App
39	0	0.0	1	10	US-09-882-171-611	Sequence 611, App
40	0	0.0	1	11	US-09-833-245-184	Sequence 184, App
41	0	0.0	1	11	US-09-833-245-186	Sequence 186, App
42	0	0.0	1	11	US-09-833-245-325	Sequence 325, App
43	0	0.0	1	11	US-09-833-245-500	Sequence 500, App
44	0	0.0	1	11	US-09-833-245-744	Sequence 744, App
45	0	0.0	1	11	US-09-833-245-1045	Sequence 1045, Ap

ALIGNMENTS

RESULT 1

US-09-778-885-5  
; Sequence 5, Application US/09778885  
; Publication No. US20020039748A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS  
; TITLE OF INVENTION: AND METHODS FOR MAKING IT  
; FILE REFERENCE: 98-22  
; CURRENT APPLICATION NUMBER: US/09/778,885  
; CURRENT FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 09/320,095  
; PRIOR FILING DATE: 1999-05-26  
; PRIOR APPLICATION NUMBER: US 60/087,032  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide motif  
; NAME/KEY: VARIANT  
; LOCATION: (2)...(2)  
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,  
; OTHER INFORMATION: Pro, Trp or Val  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Pro  
; NAME/KEY: VARIANT  
; LOCATION: (4)...(4)  
; OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp,  
; OTHER INFORMATION: Tyr or Val



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LOCATION: (5)...(5)  
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,  
OTHER INFORMATION: Ser, Thr or Trp  
NAME/KEY: VARIANT  
LOCATION: (6)...(6)  
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr  
OTHER INFORMATION: Or Met  
NAME/KEY: VARIANT  
LOCATION: (7)...(7)  
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,  
OTHER INFORMATION: Met, Phe or Trp  
NAME/KEY: VARIANT  
LOCATION: (8)...(8)  
OTHER INFORMATION: Xaa is Gly or Glu  
NAME/KEY: VARIANT  
LOCATION: (9)...(9)  
OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr  
NAME/KEY: VARIANT  
LOCATION: (11)...(11)  
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,  
OTHER INFORMATION: Pro, Trp and Val  
NAME/KEY: VARIANT  
LOCATION: (12)...(12)  
OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr  
OTHER INFORMATION: and Ser  
NAME/KEY: VARIANT  
LOCATION: (13)...(13)  
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, Thr  
OTHER INFORMATION: Or Trp  
NAME/KEY: VARIANT  
LOCATION: (14)...(14)  
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His,  
OTHER INFORMATION: Ser, Trp or Tyr  
NAME/KEY: VARIANT  
LOCATION: (15)...(15)  
OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His,  
OTHER INFORMATION: Met, Trp or Tyr  
NAME/KEY: VARIANT  
LOCATION: (16)...(16)  
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile  
NAME/KEY: VARIANT  
LOCATION: (17)...(17)  
OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu  
NAME/KEY: VARIANT  
LOCATION: (18)...(18)  
OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala  
NAME/KEY: VARIANT  
LOCATION: (19)...(19)  
OTHER INFORMATION: Xaa is Tyr or Phe  
NAME/KEY: VARIANT  
LOCATION: (20)...(20)  
OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp  
NAME/KEY: VARIANT  
LOCATION: (21)...(21)  
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr  
NAME/KEY: VARIANT  
LOCATION: (22)...(22)  
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp  
NAME/KEY: VARIANT  
LOCATION: (23)...(23)  
OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val  
NAME/KEY: VARIANT  
LOCATION: (24)...(24)  
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met  
NAME/KEY: VARIANT  
LOCATION: (25)...(25)  
OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, Tyr  
US-09-778-885-5  
Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 V 1  
RESULT 2  
US-09-909-348-4  
; Sequence 4, Application US/09909348  
; Patent No. US20020042373A1  
; GENERAL INFORMATION:  
; APPLICANT: Carney, Darrell H.  
; APPLICANT: Crowther, Roger S.  
; APPLICANT: Stierberg, Janet  
; APPLICANT: Bergmann, John  
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists  
; FILE REFERENCE: 3033.1003-001  
; CURRENT APPLICATION NUMBER: US/09/909,348  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/219,800  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide fragment of Thrombin  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(14)  
; OTHER INFORMATION: Xaa at position six is Glu or Gln  
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or  
US-09-909-348-4  
Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
Db 1 V 1  
RESULT 3  
US-09-982-172-3  
; Sequence 3, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-3  
Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1

Db 1 K 1

RESULT 4

US-09-982-172-4

; Sequence 4, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-4

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 5

US-09-982-172-9

; Sequence 9, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-9

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 6

US-09-982-172-11

; Sequence 11, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-11

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 7

US-09-982-172-19

; Sequence 19, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-19

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 8

US-09-982-172-31

; Sequence 31, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-31

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

RESULT 9

US-09-982-172-35  
; Sequence 35, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-35

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 R 1

RESULT 10

US-09-982-172-37  
; Sequence 37, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-37

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

RESULT 11  
US-09-982-172-46

; Sequence 46, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-46

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

RESULT 12

US-09-982-172-69  
; Sequence 69, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 69  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-69

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

RESULT 13

US-09-982-172-80  
; Sequence 80, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 80  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-80

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 14  
US-09-982-172-81  
; Sequence 81, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 81  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-81

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 15  
US-09-982-172-83  
; Sequence 83, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 83  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-83

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
Db 1 R 1

Search completed: December 29, 2004, 21:30:09  
Job time : 138 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:10:20 ; Search time 37 Seconds  
(without alignments)  
20.804 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 8

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	3	3 RSHST	thyroliberin - she
2	0	0.0	3	3 A92971	thyroliberin - eas
3	0	0.0	3	3 RHTDO	thyroliberin - Bom
4	0	0.0	3	3 A22565	R-phycocerythrin al
5	0	0.0	3	3 PQ0010	angiotensin-conver
6	0	0.0	3	3 S13894	histidinol dehydro
7	0	0.0	3	3 A43391	TRH-like tripeptid
8	0	0.0	3	3 E37196	bradykinin-potenti
9	0	0.0	3	3 F37196	bradykinin-potenti
10	0	0.0	3	3 I50412	gene p20K protein
11	0	0.0	3	3 PT0636	T-cell receptor be
12	0	0.0	3	3 PT0578	T-cell receptor be
13	0	0.0	3	3 PT0571	T-cell receptor be
14	0	0.0	3	3 PT0622	T-cell receptor be
15	0	0.0	3	3 I78890	tyrosine protein k
16	0	0.0	3	3 S68328	blood cell protein
17	0	0.0	3	3 T13892	cytochrome-c oxida
18	0	0.0	3	3 GKHU	growth-modulating
19	0	0.0	3	3 RHPGT	thyroliberin - pig
20	0	0.0	3	3 A60898	bursin - chicken
21	0	0.0	3	3 A23751	spinal cord peptid
22	0	0.0	3	3 B23751	spinal cord peptid
23	0	0.0	3	3 A33802	thyrotropin-releas
24	0	0.0	4	1 ECXAA	antho-RFamide neur
25	0	0.0	4	2 S18401	thyroglobulin - do
26	0	0.0	4	2 A02147	phagocytosis-stimu
27	0	0.0	4	2 A37832	phenol 2-monooxyge
28	0	0.0	4	2 A48360	gamma subunit of p
29	0	0.0	4	2 A61300	22K superhelical D

30	0	0.0	4	2 A41890	protein D - Escher
31	0	0.0	4	2 S43014	hypothetical prote
32	0	0.0	4	2 D41654	hypothetical prote
33	0	0.0	4	2 B43848	cell surface adhes
34	0	0.0	4	2 I40505	hypothetical prote
35	0	0.0	4	2 I40870	phospholipase C (E
36	0	0.0	4	2 T46627	hypothetical prote
37	0	0.0	4	2 S53508	starvation-induced
38	0	0.0	4	2 A27897	glucan 1,4-alpha-g
39	0	0.0	4	2 T30569	hypothetical prote
40	0	0.0	4	2 I38888	COI intron 16 prot
41	0	0.0	4	2 A25844	autho-RF amide neu
42	0	0.0	4	2 A34626	RPCB-related neuro
43	0	0.0	4	2 I51049	metallothionein-A
44	0	0.0	4	2 S39390	myosin-light-chain
45	0	0.0	4	2 I61883	protamine P1 - ora

ALIGNMENTS

RESULT 1

RHSHT

thyroliberin - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C;Accession: A93750; A01415

R;Desiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

Org. Mass Spectrom. 5, 221-228, 1971

A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating

A;Reference number: A93750

A;Accession: A93750

A;Molecule type: protein

A;Residues: 1-3 <DES>

A;Cross-references: UNIPROT:P01151

R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.

A;Reference number: A93161; MUID:70163386; PMID:4985794

A;Contents: annotation

A;Note: physicochemical characteristics and biological activities of the natural and synt

C;Superfamily: thyroliberin

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match	0.0%;	Score 0;	DB 3;	Length 3;
Best Local Similarity	0.0%;	Pred. No. 0;		
Matches	0;	Conservative	0;	Mismatches 1;
Indels			0;	Gaps 0;

QY 1 X 1

Db 1 Q 1

RESULT 2

A92971

thyroliberin - eastern newt (tentative sequence)

C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C;Accession: A92971; A01415

R;Grimm-Jorgensen, Y.; McKelvy, J.F.

J. Neurochem. 23, 471-478, 1974

A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brai

A;Reference number: A92971; MUID:75035605; PMID:4214528

A;Accession: A92971

A;Molecule type: protein

A;Residues: 1-3 <GRI>

A;Cross-references: UNIPROT:P01151

A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyroli

stidine, or glutamic acid

C;Superfamily: thyroliberin

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic a

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 3  
RHTDFO  
thyroliberin - Bombina orientalis  
C:Species: Bombina orientalis  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004  
C:Accession: A90919; A01415  
R:Yasuhara, T.; Nakajima, T.  
Chem. Pharm. Bull. 23, 3301-3303, 1975  
A:Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.  
A:Reference number: A90919; MUID:76138399; PMID:815011  
A:Accession: A90919  
A:Molecule type: protein  
A:Residues: 1-3 <YAS>  
A:Cross-references: UNIPROT:P01151  
C:Superfamily: thyroliberin  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 4  
A22565  
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C:Species: Gastroclonium coulteri  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601; PMID:3886644  
A:Accession: A22565  
A:Molecule type: protein  
A:Residues: 1-3 <KLO>

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 2 Y 2

RESULT 5  
PQ0010  
angiotensin-converting enzyme inhibitor (FLP-3) - common fig  
N:Alternate names: ficus latex peptide 3  
C:Species: Ficus carica (common fig)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: PQ0010  
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A:Reference number: PQ0008  
A:Accession: PQ0010  
A:Molecule type: protein  
A:Residues: 1-3 <MAR>  
A:Experimental source: latex  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 L 1

RESULT 6  
S13894  
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)  
C:Species: Brassica oleracea (wild cabbage)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: S13894  
R:Nagai, A.; Scheidegger, A.  
Arch. Biochem. Biophys. 284, 127-132, 1991  
A:Title: Purification and characterization of histidinol dehydrogenase from cabbage.  
A:Reference number: S13894; MUID:91112783; PMID:1989490  
A:Accession: S13894  
A:Molecule type: protein  
A:Residues: 1-3 <NAG>  
A:Experimental source: var. capitata  
C:Keywords: dimer; NAD; oxidoreductase

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 X 1

RESULT 7  
A43391  
TRH-like tripeptide - alfalfa  
C:Species: Medicago sativa (alfalfa)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A43391  
R:Jackey, D.B.  
J. Biol. Chem. 267, 17508-17511, 1992  
A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-  
A:Reference number: A43391; MUID:92388092; PMID:1517203  
A:Accession: A43391  
A:Molecule type: protein  
A:Residues: 1-3 <LAC>  
C:Keywords: amidated carboxyl end; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 8  
E37196  
bradykinin-potentiating peptide 5 - island jararaca  
C:Species: Bothrops insularis (island jararaca)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 30-Jun-2001  
C:Accession: E37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: E37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-3 <CIN>  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 9  
F37196  
bradykinin-potentiating peptide 6 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: F37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: F37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-3 <CIN>  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 10  
I50412  
gene p20K protein - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I50412  
R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.  
J. Biol. Chem. 268, 8131-8139, 1993  
A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken  
A;Reference number: A46643; MUID:93216790; PMID:8463325  
A;Accession: I50412  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <MAO>  
A;Cross-references: GB:L02537; NID:g212616; PID:g212617  
C;Genetics:  
A;Gene: p20K

RESULT 11  
PT0636  
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0636  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0636  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 A 1

RESULT 12  
PT0578  
T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0578  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0578  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 A 1

RESULT 13  
PT0571  
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0571  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0571  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 A 1

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 2 S 2

Qy 1 X 1  
Db 1 A 1

RESULT 14  
PT0622  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0622; PT0680; PT0582; PT0673  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0622  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P  
A;Accession: PT0680  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-3 <FEE1>  
A;Experimental source: day 18 fetal thymus, strain BALB/c clones 154-1J and 154-1F  
A;Accession: PT0582  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE2>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 A 1

RESULT 15  
I78890  
tyrosine protein kinase - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I78890  
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
Oncogene 9, 3437-3448, 1994  
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein  
A;Reference number: I58407; MUID:95060800; PMID:7970703  
A;Accession: I78890  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <RES>  
A;Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538  
C;Genetics:  
A;Gene: p52ntk

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 3 T 3

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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:01:44 ; Search time 185 Seconds  
(without alignments)  
24.881 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 835

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	0	0.0	2	1	GWA_SEPOF	P83570 sepia offic
2	0	0.0	3	1	GRWM_HUMAN	P01157 homo sapien
3	0	0.0	3	1	LUXE_VIBFI	P24272 vibrio fisc
4	0	0.0	3	1	THYL_PIG	P01151 sus scrofa
5	0	0.0	4	1	ACH1_ACHFU	P35904 achatina fu
6	0	0.0	4	1	DCML_PSECH	P19916 pseudomonas
7	0	0.0	4	1	DCMS_PSECH	P19918 pseudomonas
8	0	0.0	4	1	EOSI_HUMAN	P02731 homo sapien
9	0	0.0	4	1	FAR3_HIRME	P42562 hirudo medi
10	0	0.0	4	1	FAR4_HIRME	P42563 hirudo medi
11	0	0.0	4	1	FFKA_ATEL	P58705 anthopleura
12	0	0.0	4	1	FLRF_HIRME	P42561 hirudo medi
13	0	0.0	4	1	FLRN_ATEL	P58707 anthopleura
14	0	0.0	4	1	FMRF_MACNI	P01162 macrocallis
15	0	0.0	4	1	FYRI_ATEL	P58706 anthopleura
16	0	0.0	4	1	ILME_SEPOF	P83568 sepia offic
17	0	0.0	4	1	OCPI_OCTMI	P58648 octopus min
18	0	0.0	4	1	OCPI_OCTMI	P58649 octopus min
19	0	0.0	4	1	TUFT_HUMAN	P01858 homo sapien
20	0	0.0	4	1	YLM1_YEAST	P36515 saccharomyc
21	0	0.0	4	2	Q16047	Q16047 homo sapien
22	0	0.0	4	2	Q96AT0	Q96AT0 homo sapien
23	0	0.0	4	2	Q08433	Q08433 rattus sp.
24	0	0.0	5	1	AL14_CARMA	P81817 carcinus ma
25	0	0.0	5	1	BIOA_CITFR	P13071 citrobacter
26	0	0.0	5	1	BIOB_CITFR	P12997 citrobacter
27	0	0.0	5	1	BPP7_BOTIN	P30425 bothrops in
28	0	0.0	5	1	EI03_LITRU	P82099 litoria rub
29	0	0.0	5	1	EI04_LITRU	P82100 litoria rub
30	0	0.0	5	1	FARP_ARTTR	P41853 artiopesthi
31	0	0.0	5	1	FARP_CHICK	P83308 gallus gall

32	0	0.0	5	1	MPA4_JUNVI	P81826 juniperus v
33	0	0.0	5	1	PAP2_PARMA	P81864 pardachirus
34	0	0.0	5	1	PRCT_PERAM	P01373 periplaneta
35	0	0.0	5	1	PSK_DAUCA	P58261 daucus caro
36	0	0.0	5	1	RE11_LITRU	P82070 litoria rub
37	0	0.0	5	1	RE21_LITRU	P82071 litoria rub
38	0	0.0	5	1	RE31_LITRU	P82072 litoria rub
39	0	0.0	5	1	RE32_LITRU	P82073 litoria rub
40	0	0.0	5	1	SUGA_ACHDO	P19991 acheta dome
41	0	0.0	5	1	TPIS_CANFA	P54714 canis famil
42	0	0.0	5	1	TRM3_ECOLI	P13973 escherichia
43	0	0.0	5	1	UC22_MAIZE	P80628 zea mays (m
44	0	0.0	5	1	UF01_MOUSE	P38639 mus musculu
45	0	0.0	5	1	UXA4_CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1  
GWA\_SEPOF  
ID GWA\_SEPOF STANDARD; PRT; 2 AA.  
AC P83570;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide GWA.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX MEDLINE=98100358; PubMed=9437704;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
RT peptide inhibiting the motility of the mature oviduct in the  
RT cuttlefish, Sepia officinalis.";  
RL Peptides 18:1469-1474(1997).  
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity  
CC targeting the distal oviduct. Inhibits the motility of the oviduct  
CC by decreasing tonus, frequency and amplitude of contractions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 2 Tryptophan amide.  
SQ SEQUENCE 2 AA; 261 MW; 737810000000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 2;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 G 1

RESULT 2  
GRWM\_HUMAN  
ID GRWM\_HUMAN STANDARD; PRT; 3 AA.  
AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Growth-modulating peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77162369; PubMed=858356;



RA Schlesinger D.H., Pickart L., Thaler M.M.;  
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
RL Experientia 33:324-325(1977).  
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
CC growth of some cell types and to inhibit other types in vitro.  
DR GO; GO:0001558; P:regulation of cell growth; NAS.  
KW Direct protein sequencing.  
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 3;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 G 1  
  
RESULT 3  
LUXE\_VIBFI STANDARD; PRT; 3 AA.  
ID LUXE\_VIBFI  
AC P24272;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-  
DE protein synthetase) (Fragment).  
GN Name=luxe;  
OS Vibrio fischeri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91072226; PubMed=22542556;  
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;  
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination  
RT site for the lux operon.";  
RL J. Bacteriol. 172:6797-6802(1990).  
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It  
CC is a component of the fatty acid reductase complex responsible for  
CC converting tetradecanoic acid to the aldehyde which serves as  
CC substrate in the luciferase-catalyzed reaction.  
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +  
CC an acyl-protein thiolester.  
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.  
CC -!- SIMILARITY: Belongs to the luxE family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; M62812; -; NOT ANNOTATED\_CDS.  
KW Ligase; Luminescence.  
FT NON TER 1  
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 3;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 I 1  
  
RESULT 4  
THYL\_PIG STANDARD; PRT; 3 AA.  
ID THYL\_PIG

AC P01151;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).  
OS Sus scrofa (Pig);  
OS Ovis aries (Sheep);  
OS Bombina orientalis (Oriental fire-bellied toad), and  
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823, 9940, 8346, 8316;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Pig; TISSUE=Hypothalamus;  
RX MEDLINE=70136150; PubMed=4984938;  
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;  
RT "Structure of porcine thyrotropin releasing hormone.";  
RL Biochemistry 9:1103-1106(1970).  
RN [2]  
RP SYNTHESIS.  
RC SPECIES=Pig;  
RX MEDLINE=70039904; PubMed=4982117;  
RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
RT "The identity of chemical and hormonal properties of the thyrotropin  
RT releasing hormone and pyroglutamyl-histidyl-proline amide.";  
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=Sheep; TISSUE=Hypothalamus;  
RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,  
RA Ward D.N.;  
RT "The elucidation of the primary structure of the hypothalamic thyroid  
RT stimulating hormone releasing factor of ovine origin by means of mass  
RT spectrometry.";  
RL Org. Mass Spectrom. 5:221-228(1971).  
RN [4]  
RP SYNTHESIS.  
RC SPECIES=Sheep;  
RX MEDLINE=70163386; PubMed=4985794;  
RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,  
RA Guillemin R.;  
RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing  
RT factor.";  
RL Nature 226:321-325(1970).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=B.orientalis; TISSUE=Skin;  
RX MEDLINE=76138399; PubMed=815011;  
RA Yasuhara T., Nakajima T.;  
RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";  
RL Chem. Pharm. Bull. 23:3301-3303(1975).  
RN [6]  
RP SEQUENCE.  
RC SPECIES=N.viridescens;  
RX MEDLINE=75035605; PubMed=4214528;  
RA Grimm-Joergensen Y., McKelvy J.F.;  
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus  
RT viridescens) brain in vitro. Isolation and characterization of  
RT thyrotropin releasing factor.";  
RL J. Neurochem. 23:471-478(1974).  
CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH  
CC in the anterior pituitary gland and as a neurotransmitter/  
CC neuromodulator in the central and peripheral nervous systems.  
DR PIR; A90919; RHTDTO.  
DR PIR; A92971; A92971.  
DR PIR; A93750; RSHST.  
KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 3 3 Proline amide.  
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 5  
ACH1\_ACHFUFU  
ID ACH1\_ACHFUFU STANDARD; PRT; 4 AA.  
AC P35904;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Achatin-I.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
RC STRAIN=Ferussac; TISSUE=Ganglion;  
RX MEDLINE=89273551; PubMed=2597281;  
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
fulica Ferussac containing a D-amino acid residue.";  
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=Ferussac; TISSUE=Heart atrium;  
RX MEDLINE=91264856; PubMed=1675568;  
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
RT "Purification of achatin-I from the atria of the African giant snail,  
Achatina fulica, and its possible function.";  
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=93014529; PubMed=1399265;  
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
Iwashita T., Nomoto K.;  
RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid  
residue.";  
RL Int. J. Pept. Protein Res. 39:258-264(1992).  
CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
and produces a spike broadening of the identified heart excitatory  
neuron (PON); also enhances the amplitude and frequency of the  
heart beat. Has also an effect on several other muscles.  
DR PIR; A32480; A32480.  
KW D-amino acid; Direct protein sequencing; Hormone.  
FT MOD\_RES 2 D-phenylalanine.  
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1  
Db 3 A 3

RESULT 6  
DCML\_PSECH  
ID DCML\_PSECH STANDARD; PRT; 4 AA.  
AC P19916;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
dehydrogenase subunit L) (CO-DH L) (Fragment).  
GN Name=cutL;  
OS Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae.  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
RT "Homology and distribution of CO dehydrogenase structural genes in  
carboxydotrophic bacteria.";  
RL Arch. Microbiol. 152:335-341(1989).  
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
dioxide.  
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
CC -!- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1  
molybdopterin cytosine dinucleotide (MCD) per subunit.  
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
subunit.  
DR PIR; PL0140; PL0140.  
KW Direct protein sequencing; Molybdenum; Oxidoreductase.  
FT NON\_TER 4  
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1  
Db 1 M 1

RESULT 7  
DCMS\_PSECH  
ID DCMS\_PSECH STANDARD; PRT; 4 AA.  
AC P19918;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO  
dehydrogenase subunit S) (CO-DH S) (Fragment).  
GN Name=cutS;  
OS Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae.  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
RT "Homology and distribution of CO dehydrogenase structural genes in  
carboxydotrophic bacteria.";  
RL Arch. Microbiol. 152:335-341(1989).  
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
dioxide.  
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
CC -!- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).  
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
subunit.  
DR PIR; PL0146; PL0146.  
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;  
KW Oxidoreductase.  
FT NON\_TER 4  
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 2 A 2

RESULT 8

EOSI\_HUMAN STANDARD; PRT; 4 AA.

ID EOSI\_HUMAN

AC P02731;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Eosinophilotactic peptides.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=76078412; PubMed=1060093;

RA Goetzl E.J., Austen K.F.;

RT "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";

RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

CC -|- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

DR GO:0006935; P:chemotaxis; IDA.

DR GO:0006955; P:immune response; IDA.

KW Direct protein sequencing.

FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).

FT /FTID=VAR\_005201.

SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 3 S 3

RESULT 9

FAR3\_HIRME STANDARD; PRT; 4 AA.

ID FAR3\_HIRME

AC P42562;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRFamide-like neuropeptide YLRF-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI\_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD\_RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 3 S 3

RESULT 10

FAR4\_HIRME STANDARD; PRT; 4 AA.

ID FAR4\_HIRME

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRFamide-like neuropeptide YMRF-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI\_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD\_RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Y 1

RESULT 11

FFKA\_ANTEL STANDARD; PRT; 4 AA.

ID FFKA\_ANTEL

AC P58705;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Antho-KAamide.

OS Anthopleura elegantissima (Sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

OC Nynanthaeae; Actiniidae; Anthopleura.

OX NCBI\_TaxID=6110;

RN [1]

RP SEQUENCE.

RX MEDLINE=92028852; PubMed=1681803;

RA Nothacker H.-P., Rinehart K.L. Jr., Grimmlikhuijzen C.J.P.;

RT "Isolation of L-3-phenyllactyl-Phe-Iys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";

RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).

RN [2]

RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;

RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmlikhuijzen C.J.P.;

RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).

CC -|- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- TISSUE SPECIFICITY: Neuron specific.

DR PIR; JQ1273; JQ1273.

KW Amidation; Direct protein sequencing; Neuropeptide.

QY 1 X 1

Db 1 Y 1

RESULT 10

FAR4\_HIRME STANDARD; PRT; 4 AA.

ID FAR4\_HIRME

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRFamide-like neuropeptide YMRF-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI\_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD\_RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Y 1

RESULT 11

FFKA\_ANTEL STANDARD; PRT; 4 AA.

ID FFKA\_ANTEL

AC P58705;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Antho-KAamide.

OS Anthopleura elegantissima (Sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

OC Nynanthaeae; Actiniidae; Anthopleura.

OX NCBI\_TaxID=6110;

RN [1]

RP SEQUENCE.

RX MEDLINE=92028852; PubMed=1681803;

RA Nothacker H.-P., Rinehart K.L. Jr., Grimmlikhuijzen C.J.P.;

RT "Isolation of L-3-phenyllactyl-Phe-Iys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";

RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).

RN [2]

RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;

RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmlikhuijzen C.J.P.;

RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).

CC -|- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- TISSUE SPECIFICITY: Neuron specific.

DR PIR; JQ1273; JQ1273.

KW Amidation; Direct protein sequencing; Neuropeptide.

```
FT  MOD_RES      1      1      3-phenyllactic acid.
FT  MOD_RES      4      4      Alanine amide.
SQ  SEQUENCE     4 AA;  512 MW;  6DD339C9A0000000 CRC64;

Query Match
Best Local Similarity  0.0%; Score 0; DB 1; Length 4;
Matches  0; Conservative  0; Mismatches  1; Indels  0; Gaps  0;

QY      1 X 1
Db      4 A 4

RESULT 12
FLRF_HIRME
ID  FLRF_HIRME      STANDARD;      PRT;      4 AA.
AC  P42561;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  FLRFamide.
OS  Hirudo medicinalis (Medicinal leech), and
OS  Helisoma trivolvis (Snail).
OC  Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC  Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX  NCBI_TaxID=6421, 27815;
RN  [1]
RP  SEQUENCE.
RC  SPECIES=H.medicinalis;
RX  MEDLINE=92195954; PubMed=1686933;
RA  Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT  "Identification of RFamide neuropeptides in the medicinal leech.";
RL  Peptides 12:897-908(1991).
RN  [2]
RP  SEQUENCE.
RC  SPECIES=H.trivolvis; TISSUE=Kidney;
RX  MEDLINE=94286417; PubMed=7912428;
RA  Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT  "FMRamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL  Peptides 15:31-36(1994).
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
KW  Amidation; Direct protein sequencing; Neuropeptide.
FT  MOD_RES      4      4      Phenylalanine amide.
SQ  SEQUENCE     4 AA;  582 MW;  69D40729A0000000 CRC64;

Query Match
Best Local Similarity  0.0%; Score 0; DB 1; Length 4;
Matches  0; Conservative  0; Mismatches  0; Indels  1; Gaps  0;

QY      1 X 1
Db      1 F 1

RESULT 13
FLRN_ANTLR
ID  FLRN_ANTLR      STANDARD;      PRT;      4 AA.
AC  P58707;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Antho-RNamide.
OS  Anthopleura elegantissima (Sea anemone).
OC  Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC  Nynanthaeae; Actiniidae; Anthopleura.
OX  NCBI_TaxID=6110;
RN  [1]
RP  SEQUENCE, AND MASS SPECTROMETRY.
RX  MEDLINE=90319122; PubMed=1973541;
RA  Gimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
```

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RA  Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT  "Isolation of L-3-phenyllactyl-Leu-Arg-Aen-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL  Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- TISSUE SPECIFICITY: Neuron specific.
CC  -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
DR  PIR; A35779; A35779.
KW  Amidation; Direct protein sequencing; Neuropeptide.
FT  MOD_RES      1      1      3-phenyllactic acid.
FT  MOD_RES      4      4      Asparagine amide.
SQ  SEQUENCE     4 AA;  549 MW;  64540729A0000000 CRC64;

Query Match
Best Local Similarity  0.0%; Score 0; DB 1; Length 4;
Matches  0; Conservative  0; Mismatches  1; Indels  0; Gaps  0;

QY      1 X 1
Db      1 F 1

RESULT 14
FMRF_MACNI
ID  FMRF_MACNI      STANDARD;      PRT;      4 AA.
AC  P01162;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS  Macrocallista nimbosa (Sun-ray clam),
OS  Nereis virens (Sandworm),
OS  Hirudo medicinalis (Medicinal leech), and
OS  Helisoma trivolvis (Snail).
OC  Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC  Veneroidea; Veneridae; Macrocallista.
OX  NCBI_TaxID=6594, 6353, 6421, 27815;
RN  [1]
RP  SEQUENCE, AND SYNTHESIS.
RC  SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
RX  MEDLINE=77215956; PubMed=877582;
RA  Price D.A., Greenberg M.J.;
RT  "Structure of a molluscan cardioexcitatory neuropeptide.";
RL  Science 197:670-671(1977).
RN  [2]
RP  SEQUENCE, AND CHARACTERIZATION.
RC  SPECIES=M.nimbosa; TISSUE=Ganglion;
RX  MEDLINE=78012038; PubMed=909875;
RA  Price D.A., Greenberg M.J.;
RT  "Purification and characterization of a cardioexcitatory neuropeptide
from the central ganglia of a bivalve mollusc.";
RL  Prep. Biochem. 7:261-281(1977).
RN  [3]
RP  SEQUENCE.
RC  SPECIES=N.virens;
RX  MEDLINE=90259866; PubMed=2342992;
RA  Krajniak K.G., Price D.A.;
RT  "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL  Peptides 11:75-77(1990).
RN  [4]
RP  SEQUENCE.
RC  SPECIES=H.medicinalis;
RX  MEDLINE=92195954; PubMed=1686933;
RA  Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT  "Identification of RFamide neuropeptides in the medicinal leech.";
RL  Peptides 12:897-908(1991).
RN  [5]
RP  SEQUENCE.
RC  SPECIES=H.trivolvis; TISSUE=Kidney;
RX  MEDLINE=94286417; PubMed=7912428;
RA  Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT  "FMRamide-related peptides from the kidney of the snail, Helisoma
```



Job time : 187 secs

RT trivolis.";  
RL Peptides 15:31-36(1994).  
CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
CC activities include augmentation, induction, and regularization of  
CC cardiac contraction.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
CC family.  
DR PIR; A01426; ECKK.  
DR PIR; A60418; A60418.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 F 1

RESULT 15  
FYRI\_ ANTEL STANDARD; PRT; 4 AA.  
AC P58706;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antho-Riamide I [Contains: Antho-Riamide II].  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92270459; PubMed=1821096;  
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
RA Grimmelikhuijzen C.J.P.;  
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-  
RT phenyllactyl fragment Tyr-Arg-Ile-NH2.";  
RL Peptides 12:1165-1173(1991).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=93391436; PubMed=8397415;  
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
RT "The expansion behaviour of sea anemones may be coordinated by two  
RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";  
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).  
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
CC groups. May be involved in the expansion phase of feeding  
CC behaviour in sea anemones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Neuron specific.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT CHAIN 1 4 Antho-Riamide I.  
FT CHAIN 2 4 Antho-Riamide II.  
FT MOD\_RES 1 1 3-phenyllactic acid.  
FT MOD\_RES 4 4 Isoleucine amide.  
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 F 1



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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 55.6981 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	2	ADD95004 Platelet
2	0	0.0	1	2	ADD94992 Platelet
3	0	0.0	1	2	ADD94993 Platelet
4	0	0.0	1	2	ADD95002 Platelet
5	0	0.0	1	2	ADD94997 Platelet
6	0	0.0	1	2	ADD94999 Platelet
7	0	0.0	1	2	ADD95003 Platelet
8	0	0.0	1	2	ADD94995 Platelet
9	0	0.0	1	2	ADD94998 Platelet
10	0	0.0	1	2	ADD95001 Platelet
11	0	0.0	1	2	ADD94990 Platelet
12	0	0.0	1	2	ADD94991 Platelet
13	0	0.0	1	2	ADD94994 Platelet
14	0	0.0	1	2	ADD94996 Platelet
15	0	0.0	1	2	ADD95000 Platelet
16	0	0.0	1	2	AAY46652 Immunogen
17	0	0.0	1	4	AAM97834 Human pep
18	0	0.0	1	4	AAM97974 Human pep
19	0	0.0	1	4	AAM97643 Human pep
20	0	0.0	1	4	AAM98447 Human pep
21	0	0.0	1	4	AAM98354 Human pep
22	0	0.0	1	4	AAM53290 Human non
23	0	0.0	1	4	AAM53329 Human non
24	0	0.0	1	4	AAM53291 Human non
25	0	0.0	1	4	AAM53328 Human non

26	0	0.0	1	4	AAM53219	Aam53219 Human non
27	0	0.0	1	4	AAM53218	Aam53218 Human non
28	0	0.0	1	4	AAB91029	Aab91029 Thyrotrop
29	0	0.0	1	4	AAB91739	Aab91739 Oploid pe
30	0	0.0	1	4	AAB92150	Aab92150 Polypepti
31	0	0.0	1	4	AAB91892	Aab91892 Apoptosis
32	0	0.0	1	4	AAB91546	Aab91546 Endotheli
33	0	0.0	1	4	AAB92392	Aab92392 Miscellan
34	0	0.0	1	4	AAB91665	Aab91665 Oploid pe
35	0	0.0	1	4	AAG99966	Aag99966 ERA bindi
36	0	0.0	1	4	AAM00011	Aam00011 ERA bindi
37	0	0.0	1	4	AAG99987	Aag99987 ERA bindi
38	0	0.0	1	4	AAG99983	Aag99983 ERA bindi
39	0	0.0	1	4	AAM00013	Aam00013 ERA bindi
40	0	0.0	1	4	AAM00016	Aam00016 ERA bindi
41	0	0.0	1	4	AAG99988	Aag99988 ERA bindi
42	0	0.0	1	4	AAM00010	Aam00010 ERA bindi
43	0	0.0	1	4	ABB66809	Abb66809 Drosophil
44	0	0.0	1	4	ABB66810	Abb66810 Drosophil
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ALIGNMENTS

RESULT 1  
ADD95004  
ID ADD95004 standard; peptide; 1 AA.  
XX  
AC ADD95004;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #146.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 11; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

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ID ADD94992 standard; peptide; 1 AA.  
XX  
AC ADD94992;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #134.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
XX WPI; 1995-060950/08.  
DR  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 3  
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ID ADD94993 standard; peptide; 1 AA.  
XX  
AC ADD94993;

XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #135.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
XX WPI; 1995-060950/08.  
DR  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 4  
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ID ADD95002 standard; peptide; 1 AA.  
XX  
AC ADD95002;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #144.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10-11; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 R 1  
  
RESULT 5  
ADD94997  
ID ADD94997 standard; peptide; 1 AA.  
XX  
AC ADD94997;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #139.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
FT defined)"  
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PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 R 1  
  
RESULT 5  
ADD94997  
ID ADD94997 standard; peptide; 1 AA.  
XX  
AC ADD94997;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #139.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
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XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain

PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 R 1  
  
RESULT 6  
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ID ADD94999 standard; peptide; 1 AA.  
XX  
AC ADD94999;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #141.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
FT defined)"  
XX  
PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

RESULT 7
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AC  ADD95003;
XX
DT  29-JAN-2004 (first entry)
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DE  Platelet aggregation inhibitor peptide #145.
XX
KW  platelet aggregation inhibitor; guanidino group; amidino group.
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OS  Unidentified.
XX
FH  Key      Location/Qualifiers
FT  Modified-site 1
FT  /label= OTHER
FT  /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT  defined)"
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PN  WO9501371-A1.
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PD  12-JAN-1995.
XX
PF  22-JUN-1994; 94WO-JP0000999.
XX
PR  30-JUN-1993; 93JP-00186755.
XX
PA  (YAWA ) NIPPON STEEL CORP.
XX
PI  Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
WPI; 1995-060950/08.
XX
New RGD peptide(s) useful as anti:platelet aggregation agents - contain
guanidino or amidino gp. at N-terminal to increase stability.
XX
PD  Disclosure; Page 11; 34pp; Japanese.
XX
CC  The invention describes peptides of amino acid sequence (I) and their
CC  salts. (I) are useful as platelet aggregation inhibitors and are easily
CC  absorbed by the body. Due to the presence of the N-terminal guanidino or
CC  amidino group, (I) are provided with excellent stability so that their
CC  activity can be exhibited for an effective time after administration.
CC  Thereafter they are readily metabolised and expelled. This is the amino
CC  acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ  Sequence 1 AA;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

RESULT 8
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ID  ADD94995 standard; peptide; 1 AA.
XX
AC  ADD94995;
XX
DT  29-JAN-2004 (first entry)
XX
DE  Platelet aggregation inhibitor peptide #140.
XX
KW  platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS  Unidentified.
XX
FH  Key      Location/Qualifiers
FT  Modified-site 1
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FT  /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT  defined)"
XX
PN  WO9501371-A1.
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XX      Platelet aggregation inhibitor peptide #137.
DE
XX      platelet aggregation inhibitor; guanidino group; amidino group.
KW
XX
OS  Unidentified.
XX
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FT  Modified-site 1
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FT  /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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PN  WO9501371-A1.
XX
PD  12-JAN-1995.
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PF  22-JUN-1994; 94WO-JP0000999.
XX
PR  30-JUN-1993; 93JP-00186755.
XX
PA  (YAWA ) NIPPON STEEL CORP.
XX
PI  Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
WPI; 1995-060950/08.
XX
New RGD peptide(s) useful as anti:platelet aggregation agents - contain
guanidino or amidino gp. at N-terminal to increase stability.
XX
PD  Disclosure; Page 10; 34pp; Japanese.
XX
CC  The invention describes peptides of amino acid sequence (I) and their
CC  salts. (I) are useful as platelet aggregation inhibitors and are easily
CC  absorbed by the body. Due to the presence of the N-terminal guanidino or
CC  amidino group, (I) are provided with excellent stability so that their
CC  activity can be exhibited for an effective time after administration.
CC  Thereafter they are readily metabolised and expelled. This is the amino
CC  acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ  Sequence 1 AA;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

RESULT 9
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ID  ADD94998 standard; peptide; 1 AA.
XX
AC  ADD94998;
XX
DT  29-JAN-2004 (first entry)
XX
DE  Platelet aggregation inhibitor peptide #140.
XX
KW  platelet aggregation inhibitor; guanidino group; amidino group.
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OS  Unidentified.
XX
FH  Key      Location/Qualifiers
FT  Modified-site 1
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FT  /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT  defined)"
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PN  WO9501371-A1.
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PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
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PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
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PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 1 R 1  
  
RESULT 10  
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ID ADD95001 standard; peptide; 1 AA.  
XX  
AC ADD95001;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #143.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
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XX  
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FT defined)"  
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PN WO9501371-A1.  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #143.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
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XX  
DT 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX

PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 1 R 1  
  
RESULT 11  
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ID ADD94990 standard; peptide; 1 AA.  
XX  
AC ADD94990;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #132.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
FT defined)"  
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PN WO9501371-A1.  
XX  
DT 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
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Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 X 1  
Db 1 R 1

RESULT 12  
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XX  
AC ADD94991;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #133.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
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XX 12-JAN-1995.  
PD  
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XX 30-JUN-1993; 93JP-00186755.  
PR  
XX (YAWA ) NIPPON STEEL CORP.  
PA  
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI  
XX WPI; 1995-060950/08.  
DR  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
PT  
XX Disclosure; Page 10; 34pp; Japanese.  
PS  
XX The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
CC  
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

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XX  
AC ADD94994;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #136.

XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
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FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
FT  
XX WO9501371-A1.  
PN  
XX 12-JAN-1995.  
PD  
XX 22-JUN-1994; 94WO-JP0000999.  
PF  
XX 30-JUN-1993; 93JP-00186755.  
PR  
XX (YAWA ) NIPPON STEEL CORP.  
PA  
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI  
XX WPI; 1995-060950/08.  
DR  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
PT  
XX Disclosure; Page 10; 34pp; Japanese.  
PS  
XX The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
CC  
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Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

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XX  
AC ADD94996;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #138.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
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OS Unidentified.  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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XX WO9501371-A1.  
PN  
XX 12-JAN-1995.  
PD  
XX

PF 22-JUN-1994; 94WO-JP0000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 1 R 1  
  
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AC ADD95000;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #142.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
FT defined)"  
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PN WO9501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP0000999.  
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PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX

CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 1 R 1  
  
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Job time : 57.6981 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 18.4151 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	0	0.0	1	1	US-07-791-213D-24	Sequence 24, Appl
3	0	0.0	1	1	US-07-791-213D-40	Sequence 40, Appl
4	0	0.0	1	1	US-08-174-365A-57	Sequence 57, Appl
5	0	0.0	1	1	US-07-789-913-23	Sequence 23, Appl
6	0	0.0	1	1	US-07-789-913-25	Sequence 25, Appl
7	0	0.0	1	1	US-08-049-794-23	Sequence 23, Appl
8	0	0.0	1	1	US-08-049-794-25	Sequence 25, Appl
9	0	0.0	1	1	US-08-433-037-12	Sequence 12, Appl
10	0	0.0	1	1	US-08-448-606-4	Sequence 4, Appli
11	0	0.0	1	1	US-07-869-933-16	Sequence 16, Appl
12	0	0.0	1	1	US-08-293-150A-24	Sequence 24, Appl
13	0	0.0	1	1	US-08-293-150A-40	Sequence 40, Appl
14	0	0.0	1	1	US-08-496-847-23	Sequence 23, Appl
15	0	0.0	1	1	US-08-496-847-25	Sequence 25, Appl
16	0	0.0	1	2	US-08-742-774-23	Sequence 23, Appl
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18	0	0.0	1	2	US-08-675-354-23	Sequence 23, Appl
19	0	0.0	1	2	US-08-675-354-25	Sequence 25, Appl
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21	0	0.0	1	2	US-08-965-918-23	Sequence 23, Appl
22	0	0.0	1	2	US-08-965-918-25	Sequence 25, Appl
23	0	0.0	1	2	US-09-138-439-23	Sequence 23, Appl
24	0	0.0	1	2	US-09-138-439-25	Sequence 25, Appl
25	0	0.0	1	3	US-08-480-640A-12	Sequence 12, Appl
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38	0	0.0	1	3	US-09-392-979A-25	Sequence 25, Appl
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43	0	0.0	1	3	US-09-315-113-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1  
US-07-820-154A-12  
; Sequence 12, Application US/07820154A  
; Patent No. 5382425  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph.D., Mark D  
; APPLICANT: Junker M.S., David E  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/820,154A  
; FILING DATE: 19920113  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-820-154A-12

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Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 V 1

RESULT 2  
US-07-791-213D-24

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; Sequence 24, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; City: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-24

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 3
US-07-791-213D-40
; Sequence 40, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; City: Alexandria
; STATE: Virginia
; COUNTRY: United States
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; ZIP: 22313-1404
; COMPUTER READABLE FORM:
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-40

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 4
US-08-174-365A-57
; Sequence 57, Application US/08174365A
; Patent No. 5478809
; GENERAL INFORMATION:
; APPLICANT: Seiichi TANIDA et al.
; TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/174,365A
; FILING DATE: December 28, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acid  
TYPE: amino acid  
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LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note = "Xaa is modified amino acid as  
OTHER INFORMATION: described in specification"  
US-08-174-365A-57

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 X 1

RESULT 5  
US-07-789-913-23  
; Sequence 23, Application US/07789913  
; Patent No. 5559095  
; GENERAL INFORMATION:  
; APPLICANT: Miljanich, George P.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Fox, James A.  
; APPLICANT: Valentino, Karen L.  
; APPLICANT: Bitner, Robert S.  
; APPLICANT: Yamashiro, Donald H.  
; TITLE OF INVENTION: Delayed Treatment Method of Reducing  
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/789,913  
FILING DATE: 19911112  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/561,766  
FILING DATE: 02-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/440,094  
FILING DATE: 22-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0005.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 6  
US-07-789-913-25  
; Sequence 25, Application US/07789913  
; Patent No. 5559095  
; GENERAL INFORMATION:  
; APPLICANT: Miljanich, George P.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Fox, James A.  
; APPLICANT: Valentino, Karen L.  
; APPLICANT: Bitner, Robert S.  
; APPLICANT: Yamashiro, Donald H.  
; TITLE OF INVENTION: Delayed Treatment Method of Reducing  
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/789,913  
FILING DATE: 19911112  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/561,766  
FILING DATE: 02-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/440,094  
FILING DATE: 22-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0005.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-25

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 R 1

RESULT 7

US-08-049-794-23

; Sequence 23, Application US/08049794

; Patent No. 5587454

; GENERAL INFORMATION:

; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER

; APPLICANT: GOHIL, KISHOR C

; APPLICANT: VALENTINO, KAREN L

; APPLICANT: MILJANICH, GEORGE P

; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/049,794

; FILING DATE: 19930415

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/814,759

; FILING DATE: 30-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Stratford, Carol A.

; REGISTRATION NUMBER: 34,444

; REFERENCE/DOCKET NUMBER: 5865-0009.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE

; INDIVIDUAL ISOLATE: 32

US-08-049-794-23

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 C 1

RESULT 8

US-08-049-794-25

; Sequence 25, Application US/08049794

; Patent No. 5587454

; GENERAL INFORMATION:

; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER

; APPLICANT: GOHIL, KISHOR C

; APPLICANT: VALENTINO, KAREN L

; APPLICANT: MILJANICH, GEORGE P

; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/049,794

; FILING DATE: 19930415

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/814,759

; FILING DATE: 30-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Stratford, Carol A.

; REGISTRATION NUMBER: 34,444

; REFERENCE/DOCKET NUMBER: 5865-0009.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE

; INDIVIDUAL ISOLATE: 32

US-08-049-794-25

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 R 1

RESULT 9

US-08-433-037-12

; Sequence 12, Application US/08433037

; Patent No. 5707828

; GENERAL INFORMATION:

; APPLICANT: Sreekrishna, Kotikanyadan

; APPLICANT: Barr, Kathryn A.

; APPLICANT: Brierley, Russell A.

; APPLICANT: Thill, Gregory P.

; APPLICANT: Tschopp, Juerg F.

; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 11530-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/433,037  
FILING DATE: 03-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9108Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-433-037-12

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 1 L 1

RESULT 10

US-08-448-606-4  
Sequence 4, Application US/08448606  
Patent No. 5721114  
GENERAL INFORMATION:  
APPLICANT: Abrahams n, Lars  
APPLICANT: Holmgren, Erik  
APPLICANT: Kalder n, Christina  
APPLICANT: Lake, Mats  
APPLICANT: Mikaelsson, sa  
APPLICANT: Sejlitz, Torsten  
TITLE OF INVENTION: Expression System For Producing  
TITLE OF INVENTION: Apolipoprotein AI-M  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pollock, Vande Sande & Priddy  
STREET: 1990 M Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,606  
FILING DATE: 25-AUG-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/SE93/01061  
FILING DATE: 09-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9203753-0  
FILING DATE: 11-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Amernick, Burton A.  
REGISTRATION NUMBER: 24,852  
REFERENCE/DOCKET NUMBER: 0151/00121  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)331-7111  
TELEFAX: (202) 293-6229  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acid  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-448-606-4

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 1 Q 1

RESULT 11

US-07-869-933-16  
Sequence 16, Application US/07869933  
Patent No. 5770396  
GENERAL INFORMATION:  
APPLICANT: KINET, Jean-Pierre  
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
TITLE OF INVENTION: IMMUNOGLOBULIN  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/869,933  
FILING DATE: 19920416  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-869-933-16  
Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 1 M 1

RESULT 12

US-08-293-150A-24

Sequence 24, Application US/08293150A

; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-293-150A-24

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 13  
US-08-293-150A-40  
; Sequence 40, Application US/08293150A  
; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria

; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-293-150A-40

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 14  
US-08-496-847-23  
; Sequence 23, Application US/08496847  
; Patent No. 5795864  
; GENERAL INFORMATION:  
; APPLICANT: Amstutz, Gary A.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Gohil, Kishorchandra  
; APPLICANT: Adriaenssens, Peter I.  
; APPLICANT: Kristipati, Ramasharma  
; TITLE OF INVENTION: METHODS AND  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94306-1546  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/496,847  
; FILING DATE: 27-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A

; REGISTRATION NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 5865-0009.31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-0880  
; TELEFAX: 650-324-0960  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
US-08-496-847-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 15  
US-08-496-847-25  
; Sequence 25, Application US/08496847  
; Patent No. 5795864  
; GENERAL INFORMATION:  
; APPLICANT: Amstutz, Gary A.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Gohil, Kishorchandra  
; APPLICANT: Adriaenssens, Peter I.  
; APPLICANT: Kristipati, Ramasharma  
; TITLE OF INVENTION: METHODS AND  
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94306-1546  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/496,847  
; FILING DATE: 27-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A  
; REGISTRATION NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 5865-0009.31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-0880  
; TELEFAX: 650-324-0960  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
US-08-496-847-25

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
Db 1 R 1

Search completed: December 30, 2004, 13:19:16  
Job time : 19.4151 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 13:08:04 ; Search time 59.6226 Seconds  
(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	0	0.0	1	9	US-09-909-348-4
3	0	0.0	1	9	US-09-982-172-3
4	0	0.0	1	9	US-09-982-172-4
5	0	0.0	1	9	US-09-982-172-9
6	0	0.0	1	9	US-09-982-172-11
7	0	0.0	1	9	US-09-982-172-19
8	0	0.0	1	9	US-09-982-172-31
9	0	0.0	1	9	US-09-982-172-35
10	0	0.0	1	9	US-09-982-172-37
11	0	0.0	1	9	US-09-982-172-46
12	0	0.0	1	9	US-09-982-172-69
13	0	0.0	1	9	US-09-982-172-80

14	0	0.0	1	9	US-09-982-172-81	Sequence 81, Appl
15	0	0.0	1	9	US-09-982-172-83	Sequence 83, Appl
16	0	0.0	1	9	US-09-982-172-86	Sequence 86, Appl
17	0	0.0	1	9	US-09-982-172-93	Sequence 93, Appl
18	0	0.0	1	9	US-09-982-172-95	Sequence 95, Appl
19	0	0.0	1	9	US-09-982-172-106	Sequence 106, App
20	0	0.0	1	9	US-09-982-172-112	Sequence 112, App
21	0	0.0	1	9	US-09-982-172-120	Sequence 120, App
22	0	0.0	1	9	US-09-982-172-126	Sequence 126, App
23	0	0.0	1	9	US-09-982-172-148	Sequence 148, App
24	0	0.0	1	9	US-09-982-172-149	Sequence 149, App
25	0	0.0	1	9	US-09-982-172-155	Sequence 155, App
26	0	0.0	1	9	US-09-982-172-160	Sequence 160, App
27	0	0.0	1	9	US-09-982-172-172	Sequence 172, App
28	0	0.0	1	9	US-09-982-172-173	Sequence 173, App
29	0	0.0	1	9	US-09-982-172-175	Sequence 175, App
30	0	0.0	1	9	US-09-982-172-189	Sequence 189, App
31	0	0.0	1	9	US-09-982-172-190	Sequence 190, App
32	0	0.0	1	9	US-09-982-172-191	Sequence 191, App
33	0	0.0	1	9	US-09-982-172-195	Sequence 195, App
34	0	0.0	1	9	US-09-982-172-200	Sequence 200, App
35	0	0.0	1	9	US-09-982-172-211	Sequence 211, App
36	0	0.0	1	10	US-09-809-391-395	Sequence 395, App
37	0	0.0	1	10	US-09-809-391-611	Sequence 611, App
38	0	0.0	1	10	US-09-882-171-395	Sequence 395, App
39	0	0.0	1	10	US-09-882-171-611	Sequence 611, App
40	0	0.0	1	11	US-09-833-245-184	Sequence 184, App
41	0	0.0	1	11	US-09-833-245-186	Sequence 186, App
42	0	0.0	1	11	US-09-833-245-325	Sequence 325, App
43	0	0.0	1	11	US-09-833-245-500	Sequence 500, App
44	0	0.0	1	11	US-09-833-245-744	Sequence 744, App
45	0	0.0	1	11	US-09-833-245-1045	Sequence 1045, Ap

ALIGNMENTS

RESULT 1

US-09-778-885-5  
; Sequence 5, Application US/09778885  
; Publication No. US20020039748A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS  
; TITLE OF INVENTION: AND METHODS FOR MAKING IT  
; FILE REFERENCE: 98-22  
; CURRENT APPLICATION NUMBER: US/09/778,885  
; CURRENT FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 09/320,095  
; PRIOR FILING DATE: 1999-05-26  
; PRIOR APPLICATION NUMBER: US 60/087,032  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide motif  
; NAME/KEY: VARIANT  
; LOCATION: (2)...(2)  
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,  
; OTHER INFORMATION: Pro, Trp or Val  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Pro  
; NAME/KEY: VARIANT  
; LOCATION: (4)...(4)  
; OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp,  
; OTHER INFORMATION: Tyr or Val

; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,
; OTHER INFORMATION: Ser, Thr or Trp
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr
; OTHER INFORMATION: or Met
; NAME/KEY: VARIANT
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,
; OTHER INFORMATION: Met, Phe or Trp
; NAME/KEY: VARIANT
; LOCATION: (8)...(8)
; OTHER INFORMATION: Xaa is Gly or Glu
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr
; NAME/KEY: VARIANT
; LOCATION: (11)...(11)
; OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,
; OTHER INFORMATION: Pro, Trp and Val
; NAME/KEY: VARIANT
; LOCATION: (12)...(12)
; OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
; OTHER INFORMATION: and Ser
; NAME/KEY: VARIANT
; LOCATION: (13)...(13)
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, Thr
; OTHER INFORMATION: or Trp
; NAME/KEY: VARIANT
; LOCATION: (14)...(14)
; OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His,
; OTHER INFORMATION: Ser, Trp or Tyr
; NAME/KEY: VARIANT
; LOCATION: (15)...(15)
; OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His,
; OTHER INFORMATION: Met, Trp or Tyr
; NAME/KEY: VARIANT
; LOCATION: (16)...(16)
; OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile
; NAME/KEY: VARIANT
; LOCATION: (17)...(17)
; OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu
; NAME/KEY: VARIANT
; LOCATION: (18)...(18)
; OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
; NAME/KEY: VARIANT
; LOCATION: (19)...(19)
; OTHER INFORMATION: Xaa is Tyr or Phe
; NAME/KEY: VARIANT
; LOCATION: (20)...(20)
; OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp
; NAME/KEY: VARIANT
; LOCATION: (21)...(21)
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
; NAME/KEY: VARIANT
; LOCATION: (22)...(22)
; OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp
; NAME/KEY: VARIANT
; LOCATION: (23)...(23)
; OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val
; NAME/KEY: VARIANT
; LOCATION: (24)...(24)
; OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
; NAME/KEY: VARIANT
; LOCATION: (25)...(25)
; OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, Tyr
US-09-778-885-5
Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 V 1
RESULT 2
US-09-909-348-4
; Sequence 4, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stiernberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(14)
; OTHER INFORMATION: Xaa at position six is Glu or Gln
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or
US-09-909-348-4
Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 V 1
RESULT 3
US-09-982-172-3
; Sequence 3, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-3
Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1

Db 1 K 1

RESULT 4

US-09-982-172-4

; Sequence 4, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-4

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 5

US-09-982-172-9

; Sequence 9, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-9

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 6

US-09-982-172-11

; Sequence 11, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

US-09-982-172-11

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-11

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 7

US-09-982-172-19

; Sequence 19, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-19

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 8

US-09-982-172-31

; Sequence 31, Application US/09982172

; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

US-09-982-172-31

Query Match 0.0%; Score 0; DB 9; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-31

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 9

US-09-982-172-35  
; Sequence 35, Application US/09982172  
; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-35

Query Match

Best Local Similarity 0.0%; Score 0; DB 9; Length 1;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 10

US-09-982-172-37  
; Sequence 37, Application US/09982172  
; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 37

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-37

Query Match

Best Local Similarity 0.0%; Score 0; DB 9; Length 1;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 11  
US-09-982-172-46  
; Sequence 46, Application US/09982172  
; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 46

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-46

Query Match

Best Local Similarity 0.0%; Score 0; DB 9; Length 1;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 12

US-09-982-172-69

; Sequence 69, Application US/09982172  
; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 69

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-69

Query Match

Best Local Similarity 0.0%; Score 0; DB 9; Length 1;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 13

US-09-982-172-80

; Sequence 80, Application US/09982172  
; Patent No. US20020137119A1

; GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283



```

; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-80

Query Match      0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 K 1

RESULT 14
US-09-982-172-81
; Sequence 81, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-81

Query Match      0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 K 1

RESULT 15
US-09-982-172-83
; Sequence 83, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-83
```

```

Query Match      0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

Search completed: December 30, 2004, 13:49:58
Job time : 60.6226 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 9.20755 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	3	3 RHSHT	thyroliberin - she
2	0	0.0	3	3 A92971	thyroliberin - eas
3	0	0.0	3	3 RHTDTC	thyroliberin - Bom
4	0	0.0	3	3 A22565	R-phycoerythrin al
5	0	0.0	3	3 PQ0010	angiotensin-conver
6	0	0.0	3	3 S13894	histidinol dehydro
7	0	0.0	3	3 A43391	TRH-like tripeptid
8	0	0.0	3	3 E37196	bradykinin-potent
9	0	0.0	3	3 I50412	bradykinin-potent
10	0	0.0	3	3 PT0636	gene p20K protein
11	0	0.0	3	3 PT0578	T-cell receptor be
12	0	0.0	3	3 PT0571	T-cell receptor be
13	0	0.0	3	3 PT0622	T-cell receptor be
14	0	0.0	3	3 I78890	tyrosine protein k
15	0	0.0	3	3 S68328	blood cell protein
16	0	0.0	3	3 T13892	cytochrome-c oxida
17	0	0.0	3	3 GKHU	growth-modulating
18	0	0.0	3	3 RHPGT	thyroliberin - pig
19	0	0.0	3	3 A60898	bursin - chicken
20	0	0.0	3	3 A23751	spinal cord peptid
21	0	0.0	3	3 B23751	spinal cord peptid
22	0	0.0	3	3 A33802	thyrotropin-releas
23	0	0.0	4	1 ECXAA	antho-Rfamde neur
24	0	0.0	4	2 S18401	thyroglobulin - do
25	0	0.0	4	2 A02147	phagocytosis-stimu
26	0	0.0	4	2 A37832	phenol 2-monooxyge
27	0	0.0	4	2 A48360	gamma subunit of p
28	0	0.0	4	2 A61300	22K superhelical D

30	0	0.0	4	2 A41890	protein D - Escher
31	0	0.0	4	2 S43014	hypothetical prote
32	0	0.0	4	2 D41654	hypothetical prote
33	0	0.0	4	2 B43848	cell surface adhes
34	0	0.0	4	2 I40505	hypothetical prote
35	0	0.0	4	2 I40870	phospholipase C (E
36	0	0.0	4	2 T46627	hypothetical prote
37	0	0.0	4	2 S53508	starvation-induced
38	0	0.0	4	2 A27897	glucan 1,4-alpha-g
39	0	0.0	4	2 T30569	hypothetical prote
40	0	0.0	4	2 I38888	COI intron 16 prot
41	0	0.0	4	2 A25844	autho-RF amide neu
42	0	0.0	4	2 A34626	RPCH-related neuro
43	0	0.0	4	2 I51049	metallothionein-A
44	0	0.0	4	2 S39390	myosin-light-chain
45	0	0.0	4	2 I61883	protamine P1 - ora

ALIGNMENTS

RESULT 1

RHSHT

thyroliberin - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C;Accession: A93750; A01415

R;Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

Org. Mass Spectrom. 5, 221-228, 1971

A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating

A;Reference number: A93750

A;Accession: A93750

A;Molecule type: protein

A;Residues: 1-3 <DES>

A;Cross-references: UNIPROT:P01151

R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.

A;Reference number: A93161; MUID:70163386; PMID:4985794

A;Contents: annotation

A;Note: physicochemical characteristics and biological activities of the natural and synt

C;Superfamily: thyroliberin

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match	0.0%	Score 0;	DB 3;	Length 3;
Best Local Similarity	0.0%	Pred. No. 0;		
Matches	0;	Conservative	0;	Mismatches 1;
Indels			0;	Gaps 0;

QY 1 X 1

Db 1 Q 1

RESULT 2

A92971

thyroliberin - eastern newt (tentative sequence)

C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C;Accession: A92971; A01415

R;Grimm-Jorgensen, Y.; McKelvy, J.F.

J. Neurochem. 23, 471-478, 1974

A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) bra

A;Reference number: A92971; MUID:75035605; PMID:4214528

A;Accession: A92971

A;Molecule type: protein

A;Residues: 1-3 <GRI>

A;Cross-references: UNIPROT:P01151

A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyrol

istidine, or glutamic acid

C;Superfamily: thyroliberin

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 Q 1

RESULT 3  
RHTDTC  
thyroliberin - Bombina orientalis  
C;Species: Bombina orientalis  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: A90919; A01415  
R;Yasuhara, T.; Nakajima, T.  
Chem. Pharm. Bull. 23, 3301-3303, 1975  
A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.  
A;Reference number: A90919; MUID:76138399; PMID:815011  
A;Accession: A90919  
A;Molecule type: protein  
A;Residues: 1-3 <YAS>  
A;Cross-references: UNIPROT:P01151  
C;Superfamily: thyroliberin  
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 Q 1

RESULT 4  
A22565  
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: A22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: A22565  
A;Molecule type: protein  
A;Residues: 1-3 <KLO>

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 2 Y 2

RESULT 5  
PQ0010  
angiotensin-converting enzyme inhibitor (FLP-3) - common fig  
N;Alternate names: ficus latex peptide 3  
C;Species: Ficus carica (common fig)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PQ0010  
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A;Reference number: PQ0008  
A;Accession: PQ0010  
A;Molecule type: protein  
A;Residues: 1-3 <MAR>  
A;Experimental source: latex  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 L 1

RESULT 6  
S13894  
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)  
C;Species: Brassica oleracea (wild cabbage)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: S13894  
R;Nagai, A.; Scheidegger, A.  
Arch. Biochem. Biophys. 284, 127-132, 1991  
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.  
A;Reference number: S13894; MUID:91112783; PMID:1989490  
A;Accession: S13894  
A;Molecule type: protein  
A;Residues: 1-3 <NAG>  
A;Experimental source: var. capitata  
C;Keywords: dimer; NAD; oxidoreductase

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 X 1

RESULT 7  
A43391  
TRH-like tripeptide - alfalfa  
C;Species: Medicago sativa (alfalfa)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: A43391  
R;Lackey, D.B.  
J. Biol. Chem. 267, 17508-17511, 1992  
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-  
A;Reference number: A43391; MUID:92388092; PMID:1517203  
A;Accession: A43391  
A;Molecule type: protein  
A;Residues: 1-3 <LAC>  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 Q 1

RESULT 8  
E37196  
bradykinin-potentiating peptide 5 - island jaraaraca  
C;Species: Bothrops insularis (island jaraaraca)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 30-Jun-2001  
C;Accession: E37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: E37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-3 <CIN>  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 Q 1

RESULT 9  
F37196  
bradykinin-potentiating peptide 6 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: F37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: F37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-3 <CIN>  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 X 1  
Db 1 Q 1

RESULT 10  
I50412  
gene p20K protein - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I50412  
R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.  
J. Biol. Chem. 268, 8131-8139, 1993  
A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken  
A;Reference number: A46643; MUID:93216790; PMID:8463325  
A;Accession: I50412  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <MAO>  
A;Cross-references: GB:L02537; NID:g212616; PID:g212617  
C;Genetics:  
A;Gene: p20K

RESULT 11  
PT0636  
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0636  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0636  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 A 1

RESULT 12  
PT0578  
T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0578  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0578  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 A 1

RESULT 13  
PT0571  
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0571  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0571  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 A 1

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 X 1  
Db 2 S 2

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;



QY 1 X 1  
Db 1 A 1

RESULT 14  
PT0622  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0622; PT0680; PT0582; PT0673  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0622  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P  
A;Accession: PT0680  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-3 <FEE1>  
A;Experimental source: day 18 fetal thymus, strain BALB/c clones 154-1J and 154-1F  
A;Accession: PT0582  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE2>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 A 1

RESULT 15  
I78890  
tyrosine protein kinase - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I78890  
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
Oncogene 9, 3437-3448, 1994  
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein  
A;Reference number: I58407; MUID:95060800; PMID:7970703  
A;Accession: I78890  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <RES>  
A;Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538  
C;Genetics:  
A;Gene: p52ntk

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 3 T 3

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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 73.8113 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	2	1 GWA SEPOF	P83570 sepia offic
2	0	0.0	3	1 GRWM HUMAN	P01157 homo sapien
3	0	0.0	3	1 LUXE VIBFI	P24272 vibrio fisc
4	0	0.0	3	1 THYL_PIG	P01151 sus scrofa
5	0	0.0	4	1 ACHI_ACHFU	P35904 achatina fu
6	0	0.0	4	1 DCML_PSECH	P19916 pseudomonas
7	0	0.0	4	1 DCMS_PSECH	P19918 pseudomonas
8	0	0.0	4	1 EOSI_HUMAN	P02731 homo sapien
9	0	0.0	4	1 FAR3_HIRME	P42562 hirudo medi
10	0	0.0	4	1 FAR4_HIRME	P42563 hirudo medi
11	0	0.0	4	1 FFKA_ANTEL	P58705 anthopleura
12	0	0.0	4	1 FLRF_HIRME	P42561 hirudo medi
13	0	0.0	4	1 FLRN_ANTEL	P58707 anthopleura
14	0	0.0	4	1 FMRF_MACNI	P01162 macrocallis
15	0	0.0	4	1 FYRI_HUMAN	P58706 anthopleura
16	0	0.0	4	1 ILME_SEPOF	P83568 sepia offic
17	0	0.0	4	1 OCP1_OCTMI	P58648 octopus min
18	0	0.0	4	1 OCP3_OCTMI	P58649 octopus min
19	0	0.0	4	1 TUFT_HUMAN	P01858 homo sapien
20	0	0.0	4	1 YLM1_YEAST	P36515 saccharomyc
21	0	0.0	4	2 Q16047	Q16047 homo sapien
22	0	0.0	4	2 Q96AF0	Q96af0 homo sapien
23	0	0.0	4	2 Q08433	Q08433 rattus sp.
24	0	0.0	5	1 AL14_CARMA	P81817 carcinus ma
25	0	0.0	5	1 BIOA_CITFR	P13071 citrobacter
26	0	0.0	5	1 BIOB_CITFR	P12997 citrobacter
27	0	0.0	5	1 BPP7_BOTIN	P30425 bothrops in
28	0	0.0	5	1 EI03_LITRU	P82099 litoria rub
29	0	0.0	5	1 EI04_LITRU	P82100 litoria rub
30	0	0.0	5	1 FARP_ARTTR	P41853 artiposthi
31	0	0.0	5	1 FARP_CHICK	P83308 gallus gall

32	0	0.0	5	1 MPA4_JUNVI	P81826 juniperus v
33	0	0.0	5	1 PAP2_PARMA	P81864 pardachirus
34	0	0.0	5	1 PRCT_PERAM	P01373 periplaneta
35	0	0.0	5	1 PSK_DAUCA	P58261 daucus caro
36	0	0.0	5	1 RE11_LITRU	P82070 litoria rub
37	0	0.0	5	1 RE21_LITRU	P82071 litoria rub
38	0	0.0	5	1 RE31_LITRU	P82072 litoria rub
39	0	0.0	5	1 RE32_LITRU	P82073 litoria rub
40	0	0.0	5	1 SUGA_ACHDO	P19991 acheta dome
41	0	0.0	5	1 TPIS_CANFA	P54714 canis famil
42	0	0.0	5	1 TRM3_ECOLI	P13973 escherichia
43	0	0.0	5	1 UC22_MAIZE	P80628 zea mays (m
44	0	0.0	5	1 UF01_MOUSE	P38639 mus musculu
45	0	0.0	5	1 UXA4_CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1  
GWA\_SEPOF  
ID GWA\_SEPOF STANDARD; PRT; 2 AA.  
AC P83570;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide Gwa.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX MEDLINE=98100358; PubMed=9437704;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
RT peptide inhibiting the motility of the mature oviduct in the  
RT cuttlefish, Sepia officinalis.";  
RL Peptides 18:1469-1474(1997).  
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity  
CC targeting the distal oviduct. Inhibits the motility of the oviduct  
CC by decreasing tonus, frequency and amplitude of contractions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 2 Tryptophan amide.  
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 2;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 G 1

RESULT 2  
GRWM\_HUMAN  
ID GRWM\_HUMAN STANDARD; PRT; 3 AA.  
AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Growth-modulating peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77162369; PubMed=858356;

RA Schlesinger D.H., Pickart L., Thaler M.M.;  
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
RL Experientia 33:324-325(1977).  
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
CC growth of some cell types and to inhibit other types in vitro.  
DR GO; GO:0001558; P:regulation of cell growth; NAS.  
KW Direct protein sequencing.  
SQ SEQUENCE 3 AA; 340 MW; 6331E8100000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 G 1

RESULT 3  
LUXE\_VIBFI STANDARD; PRT; 3 AA.  
AC P24272;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-  
DE protein synthetase) (Fragment).  
GN Name=luxE;  
OS Vibrio fischeri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91072226; PubMed=2254256;  
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;  
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination  
RT site for the lux operon.";  
RL J. Bacteriol. 172:6797-6802(1990).  
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It  
CC is a component of the fatty acid reductase complex responsible for  
CC converting tetradecanoic acid to the aldehyde which serves as  
CC substrate in the luciferase-catalyzed reaction.  
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +  
CC an acyl-protein thiolester.  
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.  
CC -!- SIMILARITY: Belongs to the luxE family.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M62812; -; NOT\_ANNOTATED\_CDS.  
KW Ligase; Luminescence.  
FT NON\_TER 1  
SQ SEQUENCE 3 AA; 374 MW; 6AA330300000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 I 1

RESULT 4  
THYL\_PIG STANDARD; PRT; 3 AA.  
ID THYL\_PIG

AC P01151;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).  
OS Sus scrofa (Pig),  
OS Ovis aries (Sheep),  
OS Bombina orientalis (Oriental fire-bellied toad), and  
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823, 9940, 8346, 8316;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Pig; TISSUE=Hypothalamus;  
RX MEDLINE=70136150; PubMed=4984938;  
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;  
RT "Structure of porcine thyrotropin releasing hormone.";  
RL Biochemistry 9:1103-1106(1970).  
RN [2]  
RP SYNTHESIS.  
RC SPECIES=Pig;  
RX MEDLINE=70039904; PubMed=4982117;  
RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
RT "The identity of chemical and hormonal properties of the thyrotropin  
RT releasing hormone and pyroglutamyl-histidyl-proline amide.";  
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=Sheep; TISSUE=Hypothalamus;  
RX Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,  
RA Ward D.N.;  
RT "The elucidation of the primary structure of the hypothalamic thyroid  
RT stimulating hormone releasing factor of ovine origin by means of mass  
RT spectrometry.";  
RL Org. Mass Spectrom. 5:221-228(1971).  
RN [4]  
RP SYNTHESIS.  
RC SPECIES=Sheep;  
RX MEDLINE=70163386; PubMed=4985794;  
RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,  
RA Guillemin R.;  
RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing  
RT factor.";  
RL Nature 226:321-325(1970).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=B.orientalis; TISSUE=Skin;  
RX MEDLINE=76138399; PubMed=815011;  
RA Yasuhara T., Nakajima T.;  
RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";  
RL Chem. Pharm. Bull. 23:3301-3303(1975).  
RN [6]  
RP SEQUENCE.  
RC SPECIES=N.viridescens;  
RX MEDLINE=75035605; PubMed=4214528;  
RA Grimm-Joergensen Y., McKelvy J.F.;  
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus  
RT viridescens) brain in vitro. Isolation and characterization of  
RT thyrotropin releasing factor.";  
RL J. Neurochem. 23:471-478(1974).  
CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH  
CC in the anterior pituitary gland and as a neurotransmitter/  
CC neuromodulator in the central and peripheral nervous systems.  
DR PIR; A90919; RHDTDO.  
DR PIR; A92971; A92971.  
DR PIR; A93750; RSHST.  
KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 3 3 Proline amide.  
SQ SEQUENCE 3 AA; 380 MW; 7761F6B00000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 5

ACH1\_ACHFU  
ID ACH1\_ACHFU STANDARD; PRT; 4 AA.  
AC P35904;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Achatin-I.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
RC STRAIN=Ferussac; TISSUE=Ganglion;  
RX MEDLINE=89273551; PubMed=2597281;  
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
RT fulica Ferussac containing a D-amino acid residue.";  
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=Ferussac; TISSUE=Heart atrium;  
RX MEDLINE=91264856; PubMed=1675568;  
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
RT "Purification of achatin-I from the atria of the African giant snail,  
RT Achatina fulica, and its possible function.";  
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=93014529; PubMed=1399265;  
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
RA Iwashita T., Nomoto K.;  
RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
RT Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid  
RT residue.";  
RL Int. J. Pept. Protein Res. 39:258-264(1992).  
CC -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
CC and produces a spike broadening of the identified heart excitatory  
CC neuron (PON); also enhances the amplitude and frequency of the  
CC heart beat. Has also an effect on several other muscles.  
DR PIR; A32480; A32480.  
KW D-amino acid; Direct 2  
FT MOD RES 2 D-phenylalanine.  
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1  
Db 3 A 3

RESULT 6

DCML\_PSECH  
ID DCML\_PSECH STANDARD; PRT; 4 AA.  
AC P19916;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
DE dehydrogenase subunit L) (CO-DH L) (Fragment).  
GN Name=cutL;  
OS Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae.  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
RT "Homology and distribution of CO dehydrogenase structural genes in  
RT carboxydotrophic bacteria.";  
RL Arch. Microbiol. 152:335-341(1989).  
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
CC dioxide.  
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
CC -1- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1  
CC molybdopterin cytosine dinucleotide (MCD) per subunit.  
CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
CC subunit.  
DR PIR; PL0140; PL0140.  
KW Direct protein sequencing; Molybdenum; Oxidoreductase.  
FT NON TER 4  
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1  
Db 1 M 1

RESULT 7

DCMS\_PSECH  
ID DCMS\_PSECH STANDARD; PRT; 4 AA.  
AC P19918;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO  
DE dehydrogenase subunit S) (CO-DH S) (Fragment).  
GN Name=cuts;  
OS Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae.  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
RT "Homology and distribution of CO dehydrogenase structural genes in  
RT carboxydotrophic bacteria.";  
RL Arch. Microbiol. 152:335-341(1989).  
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
CC dioxide.  
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
CC -1- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).  
CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
CC subunit.  
DR PIR; PL0146; PL0146.  
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;  
KW Oxidoreductase.  
FT NON TER 4  
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1



Db 2 A 2

RESULT 8

EOSI HUMAN

ID EOSI HUMAN STANDARD; PRT; 4 AA.

AC P02731;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Eosinophilotactic peptides.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=76078412; PubMed=1060093;

RA Goetzl E.J., Austen K.F.;

RT "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";

RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

CC -!- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

CC GO:0006935; P:chemotaxis; IDA.

DR GO:0006955; P:immune response; IDA.

KW Direct protein sequencing.

FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).

FT /FTID=VAR\_005201.

SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 3 S 3

RESULT 9

FAR3\_HIRME

ID FAR3\_HIRME STANDARD; PRT; 4 AA.

AC P42562;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRFamide-like neuropeptide YLRF-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI\_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 3 S 3

RESULT 10

FAR4\_HIRME

ID FAR4\_HIRME STANDARD; PRT; 4 AA.

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRFamide-like neuropeptide YMRF-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI\_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Y 1

RESULT 11

FFKA ANTEL

ID FFKA ANTEL STANDARD; PRT; 4 AA.

AC P58705;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Antho-KAamide.

OS Anthopleura elegantissima (Sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

OC Nynanthaea; Actiniidae; Anthopleura.

OX NCBI\_TaxID=6110;

RN [1]

RP SEQUENCE.

RX MEDLINE=92028852; PubMed=1681803;

RA Nothacker H.-P., Rinehart K.L. Jr., Grimmlikhuijzen C.J.P.;

RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";

RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).

RN [2]

RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;

RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmlikhuijzen C.J.P.;

RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).

CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Neuron specific.

DR PIR; JQ1273; JQ1273.

KW Amidation; Direct protein sequencing; Neuropeptide.

QY 1 X 1

Db 1 Y 1

RESULT 10

FAR4\_HIRME

ID FAR4\_HIRME STANDARD; PRT; 4 AA.

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRFamide-like neuropeptide YMRF-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI\_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Y 1

RESULT 11

FFKA ANTEL

ID FFKA ANTEL STANDARD; PRT; 4 AA.

AC P58705;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Antho-KAamide.

OS Anthopleura elegantissima (Sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

OC Nynanthaea; Actiniidae; Anthopleura.

OX NCBI\_TaxID=6110;

RN [1]

RP SEQUENCE.

RX MEDLINE=92028852; PubMed=1681803;

RA Nothacker H.-P., Rinehart K.L. Jr., Grimmlikhuijzen C.J.P.;

RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";

RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).

RN [2]

RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;

RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmlikhuijzen C.J.P.;

RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).

CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Neuron specific.

DR PIR; JQ1273; JQ1273.

KW Amidation; Direct protein sequencing; Neuropeptide.



FT MOD\_RES 1 1 3-phenyllactic acid.  
FT MOD\_RES 4 4 Alanine amide.  
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 4 A 4  
  
RESULT 12  
FLRF\_HIRME STANDARD; PRT; 4 AA.  
AC P42561;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE FLRFamide.  
OS Hirudo medicinalis (Medicinal leech), and  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=6421, 27815;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=H.medicinalis;  
RX MEDLINE=92195954; PubMed=1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of RFamide neuropeptides in the medicinal leech.";  
RL Peptides 12:897-908(1991).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=H.trivolvis; TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma trivolvis";  
RL Peptides 15:31-36(1994).  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 1 F 1  
  
RESULT 13  
FLRN\_ANTLR STANDARD; PRT; 4 AA.  
AC P58707;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antho-RNamide.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actinidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RX MEDLINE=90319122; PubMed=1973541;  
RA Grimmelkhuizen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,

RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;  
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea anemone neuropeptide containing an unusual amino-terminal blocking group";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Neuron specific.  
CC -|- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.  
DR PIR; A35779; A35779.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 1 1 3-phenyllactic acid.  
FT MOD\_RES 4 4 Asparagine amide.  
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 1 F 1  
  
RESULT 14  
FMRF\_MACNI STANDARD; PRT; 4 AA.  
AC P01162;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).  
OS Macrocallista nimbosa (Sun-ray clam),  
OS Nereis virens (Sandworm),  
OS Hirudo medicinalis (Medicinal leech), and  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
OC Veneroidea; Veneridae; Macrocallista.  
OX NCBI\_TaxID=6594, 6353, 6421, 27815;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and visceral ganglion;  
RX MEDLINE=77215956; PubMed=877582;  
RA Price D.A., Greenberg M.J.;  
RT "Structure of a molluscan cardioexcitatory neuropeptide.";  
RL Science 197:670-671(1977).  
RN [2]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC SPECIES=M.nimbosa; TISSUE=Ganglion;  
RX MEDLINE=78012038; PubMed=909875;  
RA Price D.A., Greenberg M.J.;  
RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc";  
RL Prep. Biochem. 7:261-281(1977).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=N.virens;  
RX MEDLINE=90259866; PubMed=2342992;  
RA Krajniak K.G., Price D.A.;  
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";  
RL Peptides 11:75-77(1990).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=H.medicinalis;  
RX MEDLINE=92195954; PubMed=1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of RFamide neuropeptides in the medicinal leech.";  
RL Peptides 12:897-908(1991).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=H.trivolvis; TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma

Job time : 75.8113 secs

RT trivolis.";  
RL Peptides 15:31-36(1994).  
CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
CC activities include augmentation, induction, and regularization of  
CC cardiac contraction.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
CC family.  
DR PIR; A01426; ECKK.  
DR PIR; A60418; A60418.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 1 F 1

RESULT 15  
FYRI ANTEL  
ID -FYRI ANTEL STANDARD; PRT; 4 AA.  
AC P58706;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antho-Riamide I [Contains: Antho-Riamide II].  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynantheae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92270459; PubMed=1821096;  
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
RA Grimmelikhuijzen C.J.P.;  
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-  
RT phenyllactyl fragment Tyr-Arg-Ile-NH2.";  
RL Peptides 12:1165-1173(1991).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=93391436; PubMed=8397415;  
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
RT "The expansion behaviour of sea anemones may be coordinated by two  
RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";  
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).  
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
CC groups. May be involved in the expansion phase of feeding  
CC behaviour in sea anemones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Neuron specific.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT CHAIN 1 4 Antho-Riamide I.  
FT CHAIN 2 4 Antho-Riamide II.  
FT MOD\_RES 1 1 3-phenyllactic acid.  
FT MOD\_RES 4 4 Isoleucine amide.  
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
Db 1 F 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:19:46 ; Search time 94 Seconds  
(without alignments)  
38.163 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	61.5	10	1	AAP71548 AIDS viru
2	16	61.5	10	2	AAR28918 Peptide f
3	15	57.7	10	5	ABB46640 Desmocoll
4	15	57.7	10	5	ABB46650 Desmocoll
5	15	57.7	10	5	ABB46630 Desmocoll
6	15	57.7	10	5	ABB46621 Desmocoll
7	15	57.7	10	5	ABB47079 Desmocoll
8	15	57.7	10	5	ABB47083 Desmocoll
9	15	57.7	10	5	ABB46612 Desmocoll
10	15	57.7	10	5	ABB47075 Desmocoll
11	14	53.8	10	2	AAW09521 Thrombopo
12	14	53.8	10	2	AAW36672 Thrombopo
13	14	53.8	10	3	AAV64329 Cadherin-
14	14	53.8	10	3	AAV64331 Cadherin-
15	14	53.8	10	4	AAU25891 Human thr
16	14	53.8	10	4	AAG95975 Human com
17	14	53.8	10	4	AAG95917 Human com
18	14	53.8	10	5	ABP53955 VEGFR-3 b
19	14	53.8	10	5	ABB46625 Desmocoll
20	14	53.8	10	5	ABB46635 Desmocoll
21	14	53.8	10	5	ABB46607 Desmocoll
22	14	53.8	10	5	ABB46616 Desmocoll
23	14	53.8	10	5	ABB46645 Desmocoll
24	14	53.8	10	5	AAU93236 Granulocy
25	14	53.8	10	5	AAU98193 Prostate

26	14	53.8	10	7	ADD24107	Add24107 Melanin-c
27	14	53.8	10	8	ADH27064	Adh27064 Melanin-c
28	14	53.8	10	8	ADH27062	Adh27062 Melanin-c
29	14	53.8	10	8	ADO44204	Ado44204 Amino aci
30	14	53.8	10	8	ADP22727	Adp22727 Melanin-c
31	14	53.8	10	8	ADQ26193	Adq26193 Melanin-c
32	14	53.8	10	8	ADP71265	Adp71265 Melanin c
33	13	50.0	10	1	AAP91867	Aap91867 Cyclic pe
34	13	50.0	10	2	AAW03419	Aaw03419 Fibronect
35	13	50.0	10	2	AAW25669	Aaw25669 Mab anti-
36	13	50.0	10	2	AAW09546	Aaw09546 Thrombopo
37	13	50.0	10	2	AAW09564	Aaw09564 Thrombopo
38	13	50.0	10	2	AAW09565	Aaw09565 Thrombopo
39	13	50.0	10	2	AAW35433	Aaw35433 Thrombopo
40	13	50.0	10	2	AAW36715	Aaw36715 Thrombopo
41	13	50.0	10	2	AAW35432	Aaw35432 Thrombopo
42	13	50.0	10	2	AAW36716	Aaw36716 Thrombopo
43	13	50.0	10	2	AAW36697	Aaw36697 Thrombopo
44	13	50.0	10	2	AAW65945	Aaw65945 Molecule
45	13	50.0	10	2	AAW57567	Aaw57567 Molecular

ALIGNMENTS

RESULT 1  
AAP71548  
ID AAP71548 standard; peptide; 10 AA.  
XX  
AC AAP71548;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-MAY-1991 (first entry)  
XX  
DE AIDS virus receptor site blocking peptide (I).  
XX  
KW AIDS; virus; receptor site; HIV; vaccine; antibodies; T4 viral receptor;  
KW envelope glycoprotien; gp120; peptide T.  
XX  
OS Synthetic.  
XX  
PN EP249390-A.  
XX  
PD 16-DEC-1987.  
XX  
PF 03-JUN-1987; 87EP-00304913.  
XX  
PR 03-JUN-1986; 86US-00869919.  
PR 26-JUN-1986; 86US-00878586.  
PR 12-DEC-1986; 86US-00940919.  
PR 11-MAY-1987; 87US-00048148.  
PR 03-JUN-1987; 87EP-00304939.  
XX  
(PERT/) PERT C B.  
PA (USDC ) US SEC OF COMMERCE.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
PA (USGO ) US GOVERNMENT.  
XX  
PERT CB, Ruff MR, Farrar WL;  
XX  
WPI; 1987-350068/50.  
XX  
New peptide(s) related to AIDS virus - which inhibit AIDS virus binding  
to receptor sites and prevent cell infectivity with AIDS virus.  
PS Claim 1-2; Page 8; 12pp; English.  
XX  
The peptide may have the Cys residues at one or both the N- and C-  
terminals omitted. The resulting octapeptide in the HIV envelope  
glycoprotein (gp120) was identified by computer-assisted analysis. The  
peptide was termed "peptide T" because of the high threonine content. The  
peptide has been found to bind T4 viral receptors. The peptide blocks  
effectively receptor sites of cells and prevents cell infectivity with

CC AIDS virus in monkey, rat and human brain membranes and cells of the  
CC immune system. Vaccine prepn. contg. the peptide provide protection  
CC against infection by AIDS virus. The peptide can also be used in kits for  
CC the detection of the AIDS virus and antibodies to the AIDS virus; and as  
CC immunogens to elicit monoclonal antibodies. The peptide may be produced  
CC by conventional methods of peptide synthesis using solid phase or liquid  
CC phase methods. See also AAP71549-56, and EP-249394. (Updated on 25-MAR-  
CC 2003 to correct PA field.)  
XX  
SQ Sequence 10 AA;

Query Match 61.5%; Score 16; DB 1; Length 10;  
Best Local Similarity 20.0%; Pred. No. 28;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 1 CASTTTNYTC 10

RESULT 2  
AAR28918  
ID AAR28918 standard; peptide; 10 AA.  
XX

AC AAR28918;

XX 25-MAR-2003 (revised)  
DT 23-MAR-1993 (first entry)  
DT

XX Peptide for treating chronic fatigue syndrome.  
DE

XX CFS; fatigue; tension; anger; confusion; peptide T; HIV; synthetic;  
KW human immunodeficiency virus; gp 120.  
KW

XX Synthetic.  
OS

XX Key Location/Qualifiers  
FH Misc-difference 1 /note= "may be truncated"  
FT  
FT Misc-difference 2 /note= "Ala or D-Ala"  
FT  
FT Misc-difference 10 /note= "may be truncated"  
FT  
FT

XX WO9219257-A1.  
PN

XX 12-NOV-1992.  
PD

XX 08-MAY-1992; 92WO-US003582.  
PF

XX 08-MAY-1991; 91US-00696556.  
PR

XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
PA

XX Bridge TP, Goodwin FK;  
PI

XX WPI; 1992-398525/48.  
DR

XX Peptide compsns. for treating chronic fatigue syndrome - ameliorate  
PT symptoms and improve vigour and cognitive and neuro-motor performance.  
PT

XX Claim 1; Page 17; 2lpp; English.  
PS

XX The synthetic peptide is based on the sequence of peptide T, a sub region  
CC of HIV gp120 responsible for binding to brain membrane and human T cells.  
CC The peptide may be truncated from either end to remove cysteine residues.  
CC The peptide may be used for treatment of chronic fatigue syndrome not  
CC associated with HIV infection. The peptide will reduce fatigue, tension,  
CC anger and confusion and improves cognitive and neuromoter performance.  
CC See also AAR28919-42. (Updated on 25-MAR-2003 to correct PN field.)  
CC

XX Sequence 10 AA;  
SQ

Query Match 61.5%; Score 16; DB 2; Length 10;  
Best Local Similarity 20.0%; Pred. No. 28;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 1 CASTTTNYTC 10

RESULT 3  
ABB46640  
ID ABB46640 standard; peptide; 10 AA.  
XX

AC ABB46640;

XX 30-JAN-2002 (first entry)  
DT

XX Desmocollin-1 CAR cyclic peptide 42.  
DE

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
XX

OS Synthetic.  
OS

XX WO200172956-A2.  
PN

XX 04-OCT-2001.  
PD

XX 27-MAR-2001; 2001WO-IB001400.  
PF

XX 27-MAR-2000; 2000US-00535852.  
PR

XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA

XX Blaschuk OW, Symonds JM, Gour BJ;  
PI

XX WPI; 2002-025778/03.  
DR

XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis.  
PT

XX Claim 23; Page 109; 127pp; English.  
PS

XX The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
CC carcinoma, leukaemia or melanoma) and induce apoptosis  
XX

SQ Sequence 10 AA;

Query Match 57.7%; Score 15; DB 5; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 1 CVYAYATTAC 10

RESULT 4  
ABB46650  
ID ABB46650 standard; peptide; 10 AA.



XX ABB46650;  
AC  
XX 30-JAN-2002 (first entry)  
DT  
XX Desmocollin-1 CAR cyclic peptide 52.  
DE  
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytotostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
XX  
OS Synthetic.  
XX  
XX WO200172956-A2.  
PN  
XX 04-OCT-2001.  
PD  
XX 27-MAR-2001; 2001WO-IB001400.  
PF  
XX 27-MAR-2000; 2000US-00535852.  
PR  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA  
XX Blaschuk OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2002-025778/03.  
DR  
XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis.  
XX  
PS Claim 23; Page 109; 127pp; English.  
XX  
XX The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
CC carcinoma, leukaemia or melanoma) and induce apoptosis  
XX  
SQ Sequence 10 AA;  
  
Query Match 57.7%; Score 15; DB 5; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXC 10  
|  
Db 1 CIYAYATTAC 10  
  
RESULT 5  
ABB46630  
ID ABB46630 standard; peptide; 10 AA.  
XX  
AC ABB46630;  
XX  
XX 30-JAN-2002 (first entry)  
DT  
XX Desmocollin-1 CAR cyclic peptide 32.  
DE  
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytotostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
XX  
OS Synthetic.

XX WO200172956-A2.  
PN  
XX 04-OCT-2001.  
PD  
XX 27-MAR-2001; 2001WO-IB001400.  
PF  
XX 27-MAR-2000; 2000US-00535852.  
PR  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA  
XX Blaschuk OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2002-025778/03.  
DR  
XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis.  
XX  
PS Claim 23; Page 109; 127pp; English.  
XX  
XX The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
CC carcinoma, leukaemia or melanoma) and induce apoptosis  
XX  
SQ Sequence 10 AA;  
  
Query Match 57.7%; Score 15; DB 5; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXC 10  
|  
Db 1 CIYAYATTAC 10  
  
RESULT 6  
ABB46621  
ID ABB46621 standard; peptide; 10 AA.  
XX  
AC ABB46621;  
XX  
XX 30-JAN-2002 (first entry)  
DT  
XX Desmocollin-1 CAR cyclic peptide 23.  
DE  
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytotostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
XX  
OS Synthetic.  
XX  
XX WO200172956-A2.  
PN  
XX 04-OCT-2001.  
PD  
XX 27-MAR-2001; 2001WO-IB001400.  
PF  
XX 27-MAR-2000; 2000US-00535852.  
PR  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA  
XX Blaschuk OW, Symonds JM, Gour BJ;  
PI





Query Match 57.7%; Score 15; DB 5; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 1 CLYAYASTAC 10

RESULT 9  
ABB46612

ID ABB46612 standard; peptide; 10 AA.

XX AC ABB46612;

XX DT 30-JAN-2002 (first entry)

XX DE Desmocollin-1 CAR cyclic peptide 14.

XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytotostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.

XX OS Synthetic.

XX PN WO200172956-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-IB001400.

XX PR 27-MAR-2000; 2000US-00535852.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Symonds JM, Gour BJ;

XX DR WPI; 2002-025778/03.

XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis.

XX PS Claim 23; Page 109; 127pp; English.

XX CC The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
CC carcinoma, leukaemia or melanoma) and induce apoptosis

XX SQ Sequence 10 AA;

Query Match 57.7%; Score 15; DB 5; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 1 CAYATTADGC 10

RESULT 10  
ABB47075

ID ABB47075 standard; peptide; 10 AA.

XX AC ABB47075;

XX DT 30-JAN-2002 (first entry)

XX DE Desmocollin-3/4 CAR cyclic peptide 10.

XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytotostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.

XX OS Synthetic.

XX PN WO200172956-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-IB001400.

XX PR 27-MAR-2000; 2000US-00535852.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Symonds JM, Gour BJ;

XX DR WPI; 2002-025778/03.

XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis.

XX PS Claim 23; Page 112; 127pp; English.

XX CC The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
CC carcinoma, leukaemia or melanoma) and induce apoptosis

XX SQ Sequence 10 AA;

Query Match 57.7%; Score 15; DB 5; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 1 CAYASTADGC 10

RESULT 11  
AAW09521

ID AAW09521 standard; protein; 10 AA.

XX AC AAW09521;

XX DT 10-SEP-1997 (first entry)

XX DE Thrombopoietin receptor binding peptide.

XX KW Haematology; thrombocytopenia; TPO; TR; proliferation;  
KW bone marrow transfusion; chemotherapy; radiation therapy.

XX OS Synthetic.

XX WO9640189-A1.  
PN 19-DEC-1996.  
XX  
XX  
XX 05-JUN-1996; 96WO-US008998.  
XX  
PR 07-JUN-1995; 95US-00472371.  
PR 07-JUN-1995; 95US-00473604.  
PR 07-JUN-1995; 95US-00476168.  
PR 07-JUN-1995; 95US-00478128.  
PR 07-JUN-1995; 95US-00484090.  
PR 07-JUN-1995; 95US-00485301.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;  
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;  
XX  
DR WPI; 1997-051883/05.  
XX  
PT Thrombopoietin receptor-binding/activating peptide(s) and peptide  
PT mimetic(s) - useful in treatment of haematological disorders, esp.  
PT thrombocytopenia resulting from chemotherapy, etc.  
XX  
PS Disclosure; Page 27; 106pp; English.  
XX  
CC The present sequence is a peptide which binds to thrombopoietin (TPO)  
CC receptor (TR). The compound can be used for treating patients suffering  
CC from haematological disorders and thrombocytopenia resulting from  
CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide  
CC may also be used to maintain the proliferation and growth of TPO-  
CC dependent cell lines and for use in biological research, for detecting  
CC TPO receptors on living cells  
XX  
SQ Sequence 10 AA;  
  
Query Match 53.8%; Score 14; DB 2; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXC 10  
Db 1 CSRADFLAAC 10  
  
RESULT 12  
AAW36672  
ID AAW36672 standard; peptide; 10 AA.  
XX  
AC AAW36672;  
XX  
DT 27-FEB-1998 (first entry)  
XX  
DE Thrombopoietin receptor binding peptide.  
XX  
KW Thrombopoietin receptor; binding peptide; treatment; agonist;  
KW haematological disorder; thrombocytopenia; chemotherapy;  
KW radiation therapy; bone marrow transfusion; diagnosis;  
KW signal transduction; receptor activation; cell culture.  
XX  
OS Synthetic.  
XX  
PN WO9640750-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 07-JUN-1996; 96WO-US009623.  
XX  
PR 07-JUN-1995; 95US-00478128.  
PR 07-JUN-1995; 95US-00485301.  
XX  
PA (GLAX ) GLAXO GROUP LTD.

XX Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;  
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;  
XX  
DR WPI; 1997-052226/05.  
XX  
PT Peptides and peptide mimetics which bind to and activate the  
PT thrombopoietin receptor - useful in treatment of haematological  
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.  
XX  
PS Disclosure; Page 27; 106pp; English.  
XX  
CC The present peptide, which binds the thrombopoietin receptor (TR), can be  
CC used to treat disorders which are susceptible to treatment with a  
CC thrombopoietin agonist, preferably haematological disorders and  
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone  
CC marrow transfusions. It can also be used diagnostically, e.g. to  
CC investigate the mechanism of thrombopoietin signal transduction and  
CC receptor activation, or to maintain the proliferation and growth of  
CC thrombopoietin dependent cell lines  
XX  
SQ Sequence 10 AA;  
  
Query Match 53.8%; Score 14; DB 2; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXC 10  
Db 1 CSRADFLAAC 10  
  
RESULT 13  
AAV64329  
ID AAV64329 standard; peptide; 10 AA.  
XX  
AC AAV64329;  
XX  
DT 02-MAR-2000 (first entry)  
XX  
DE Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3644.  
XX  
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;  
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;  
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
KW neurological disease; cyclic.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 1. .10  
XX  
PN WO9957149-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 05-MAY-1999; 99WO-CA000363.  
XX  
PR 05-MAY-1998; 98US-00073040.  
PR 06-NOV-1998; 98US-00187859.  
PR 20-JAN-1999; 99US-00234395.  
PR 08-MAR-1999; 99US-00264516.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuk OW, Gour BJ, Byers S;  
XX  
DR WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin  
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid  
PT arthritis, multiple sclerosis, diabetes or a neurological disease.  
XX  
PS Claim 102; Page 218; 252pp; English.  
XX  
CC The present invention describes cadherin modulating agents (MA)  
CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
CC recognition (CAR) sequence. The MAs can be used for modulating  
CC nonclassical cadherin-mediated functions. They can be used for e.g.  
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
CC mammal, enhancing delivery of a drug through the skin of a mammal,  
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
CC expressing cell, preventing or treating obesity in a mammal, stimulating  
CC blood vessel regression in a mammal, enhancing drug delivery to the  
CC central nervous system, treating a demyelinating neurological disease,  
CC increasing vasopermeability in a mammal, enhancing adhesion of  
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing  
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a  
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age  
CC -related macular degeneration, multiple sclerosis and diabetes. The  
CC products can also be used for detection and diagnosis and in bioreactors.  
CC AAY60592 to AAY64572 represent specifically claimed peptides, and  
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in  
CC the exemplification of the present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXC 10  
Db 1 CPTIDSSGC 10  
  
RESULT 14  
AAY64331  
ID AAY64331 standard; peptide; 10 AA.  
XX  
AC AAY64331;  
XX  
DT 02-MAR-2000 (first entry)  
XX  
DE Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3646.  
XX  
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;  
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;  
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
KW neurological disease; cyclic.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 1. .10  
XX  
PN WO9957149-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 05-MAY-1999; 99WO-CA000363.  
XX

PR 05-MAY-1998; 98US-00073040.  
PR 06-NOV-1998; 98US-00187859.  
PR 20-JAN-1999; 99US-00234395.  
PR 08-MAR-1999; 99US-00264516.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuk OW, Gour BJ, Byers S;  
XX WPI; 2000-038791/03.  
DR  
XX  
PT New cadherin modulating agents, used for modulating nonclassical cadherin  
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid  
PT arthritis, multiple sclerosis, diabetes or a neurological disease.  
XX  
PS Claim 102; Page 218; 252pp; English.  
XX  
CC The present invention describes cadherin modulating agents (MA)  
CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
CC recognition (CAR) sequence. The MAs can be used for modulating  
CC nonclassical cadherin-mediated functions. They can be used for e.g.  
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
CC mammal, enhancing delivery of a drug through the skin of a mammal,  
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
CC expressing cell, preventing or treating obesity in a mammal, stimulating  
CC blood vessel regression in a mammal, enhancing drug delivery to the  
CC central nervous system, treating a demyelinating neurological disease,  
CC increasing vasopermeability in a mammal, enhancing adhesion of  
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing  
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a  
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age  
CC -related macular degeneration, multiple sclerosis and diabetes. The  
CC products can also be used for detection and diagnosis and in bioreactors.  
CC AAY60592 to AAY64572 represent specifically claimed peptides, and  
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in  
CC the exemplification of the present invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXC 10  
Db 1 CKFTIDSSC 10  
  
RESULT 15  
AAU25891  
ID AAU25891 standard; peptide; 10 AA.  
XX  
AC AAU25891;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
DE Human thrombopoietin receptor (TPO-R) activator peptide #77.  
XX  
KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;  
KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;  
KW bone marrow transplantation; haematological disorder; platelet disorder;  
KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;  
KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;  
KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.  
XX  
OS Homo sapiens.  
XX  
PN US6251864-B1.  
XX



PD 26-JUN-2001.  
XX  
PF 01-MAR-2000; 2000US-00516704.  
XX  
PR 07-JUN-1995; 95US-00478128.  
PR 07-JUN-1995; 95US-00485301.  
PR 07-JUN-1996; 96WO-US009623.  
PR 15-AUG-1996; 96US-00699027.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Dower WJ, Barrett RW, Cwirla SE, Gates CM, Schatz PJ;  
PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;  
PI Yin Q;  
XX  
DR WPI; 2001-564142/63.  
XX  
PT Activating thrombopoietin receptors in cells, used to treat  
PT thrombocytopenia and hematological disorders, comprises contacting cells  
PT with peptides and peptide mimetics attached to hydrophilic polymers.  
XX  
PS Disclosure; Col 21; 128pp; English.  
XX  
CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that  
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods  
CC of activating thrombopoietin receptors in cells comprise contacting the  
CC cells with effective amounts of peptides and peptide mimetics attached to  
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such  
CC as that due to chemotherapy, radiation therapy or bone-marrow  
CC transplantation and to prevent thrombocytopenia in patients at risk. The  
CC sequences are used to treat and prevent haematological disorders  
CC including thrombocytopenia and platelet disorders. They are used in vitro  
CC as unique tools for understanding the biological role of thrombopoietin  
CC (TPO) and to develop other compounds that bind to and activate the TPO  
CC receptor. The peptides can be used to detect TPO receptors on living  
CC cells and fixed cells, in biological fluids, in tissue homogenates, and  
CC in purified or natural biological materials. They may also be used for in  
CC situ staining, fluorescence-activated cell sorting, Western blotting and  
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can  
CC be used for in vitro expansion of megakaryocytes and their committed  
CC progenitors alone or in conjunction with additional cytokines  
XX  
SQ Sequence 10 AA;  
  
Query Match 53.8%; Score 14; DB 4; Length 10;  
Best Local Similarity 20.0%; Pred. NO. 4.8e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXXC 10  
|  
Db 1 CSRADFLAAC 10  
  
Search completed: December 29, 2004, 21:35:28  
Job time : 96.3333 secs